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OM protein - protein search, using sw model

Run on: December 2, 2004, 19:31:09 ; Search time 16 Seconds
(without alignments)
781.761 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLTETVTPNPIRFTK.....YADNDNSTGTGLLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708	100.0	244	2	JC4708
2	297.5	42.0	674	2	gelatin-binding 28
3	287.5	40.6	680	1	collagen alpha 1(X
4	280.5	39.6	674	2	collagen alpha 1(X
5	280.5	38.6	680	2	collagen alpha 1(X
6	270.5	38.6	743	1	collagen alpha 1(X
7	270.5	38.2	744	2	collagen alpha 1(X
8	267.5	37.8	744	1	collagen alpha 1(X
9	263.5	37.2	744	1	collagen alpha 1(X
10	258.5	36.5	170	2	collagen alpha 2(V
11	258.5	36.5	635	2	collagen alpha 2(V
12	243.5	34.4	619	2	hypothetical prote
13	219	30.9	245	1	complement subcomp
14	219	30.9	423	2	collagen precursor
15	208.5	29.4	246	2	complement subcomp
16	186	26.3	253	2	complement protein
17	184	26.0	253	2	complement C1q B c
18	182.5	25.8	253	1	complement subcomp
19	178	25.1	215	2	hibernation-relate
20	176	24.9	196	2	hibernation-relate
21	174	24.6	215	2	hibernation-relate
22	156	22.0	245	2	complement subcomp
23	151.5	21.4	245	1	complement subcomp
24	119.5	16.9	224	2	cerebellin-like gl
25	116.5	16.5	193	2	cerebellin precurs
26	113.5	15.0	1228	2	multimerin, endoth
27	86.5	12.2	213	2	probable protein d
28	82	11.6	280	1	phosphate ABC tran
29	77	10.9	687	2	PBSX prophage ORF

RESULT 1

JC4708
Gelatin-binding 28K protein precursor - human
N:Alternate names: adipose specific collagen-like factor
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4708; JC4944
R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.
Biochem. Biophys. Res. Commun. 221, 286-289, 1996
A:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor, af
A:Reference number: JC4708; MUID:96224171; PMID:8619847
A:Accession: JC4708
A:Molecule type: mRNA
A:Residues: 1-244 <MAX>
A:Cross-references: UNIPROT-Q15848; DDBJ-D45171; NID:g871886; PIDN:BAA08227.1; PID:g87188
A:Experimental source: adipose tissue
R:Nakano, Y.; Tober, T.; Chou-Mura, N.H.; Mazda, T.; Tomita, M.
J. Biochem. 120, 803-812, 1996
A:Title: Isolation and characterization of GSP28, a novel gelatin-binding protein purifie
A:Reference number: JC4944; MUID:97103474; PMID:8947845
A:Accession: JC4944
A:Molecule type: protein
A:Residues: 19-38;93-100;101-112;135-149;173-178 <MAX>
C:Comment: This protein is an endogenous factor that binds with a collagen-like domain. J
C:Genetics:
A:Gene: apMI
C:Keywords: adipose tissue; glycoprotein; hydroxyproline
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-244/Product: Gelatin-binding 28kDa protein #status experimental <MAT>
F:42-107/Region: collagen-like
F:114-241/Domain: complement C1q carboxyl-terminal homology <CIQ>
F:95/Modified site: 4-hydroxyproline (Pro) #status experimental
F:230/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 708; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. NO. 1.2e-63;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	FSVGLTETVTPNPIRFTKIFYNQNNHYDQSGKFKHCNIPGLYFYAYHTVTVMKDKVYS	60
Db	115	FSVGLTETVTPNPIRFTKIFYNQNNHYDQSGKFKHCNIPGLYFYAYHTVTVMKDKVYS	174
QY	61	LFKDKKAMLFYDQYQNNVDQASGVLLHLEVDQVWLVQVYGERNGLYADNDNSTF	120
Db	175	LFKDKKAMLFYDQYQNNVDQASGVLLHLEVDQVWLVQVYGERNGLYADNDNSTF	234
QY	121	TGELLYHDTN	130
Db	235	TGELLYHDTN	244

RESULT 2

S23297

collagen alpha 1(X) chain precursor - chicken

N;Alternate names: type X collagen

C;Species: Gallus gallus (chicken)

C;Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S23297; A31896; S65594; S77711; I50218

R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McG

maguchi, N.; Olsen, B.R.

in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre

A;Title: The molecular biology of collagens with short triple-helical domains.

A;Reference number: S22243

A;Accession: S23297

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-674 <NIN>

A;Cross-references: UNIPROT:P08125

R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.

J. Biol. Chem. 261, 18378-18385, 1986

A;Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and

A;Reference number: A31896; MUID:89054019; PMID:2461368

A;Accession: A31896

A;Molecule type: mRNA

A;Residues: 1-75 <LUV>

R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsemayer, T.; Olsen, B.R.

J. Biol. Chem. 261, 5041-5050, 1986

A;Title: The developmentally regulated type X collagen gene contains a long open reading

A;Reference number: I50218; MUID:86168227; PMID:3082876

A;Accession: S65594

A;Molecule type: DNA

A;Residues: 'T', '9', '11-12', 'EDOMKLYILFTM', '30-31', 'TCKSGRAFTTMYLONVMAVLVSSHT', '48-89', 'L',

629, 'PQAVLSIRWRTKSGSCQIQNPMSIPLNMFILLQSVLYLKSNIPITMS' <NINI>

A;Cross-references: EMBL:M13496; NID:G211699; PIDN:AAA48736.1; PID:G211700

A;Accession: S77711

A;Molecule type: protein

A;Residues: 104-112, 'X', '114-117', '453-466' <NIN>

A;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline;

F;1-18/Domain: signal sequence #status predicted <SIG>

F;547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>

F;453,456/Modified site: hydroxyproline (Pro) #status experimental

F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.0%; Score 297.5; DB 2; Length 674;

Best Local Similarity 47.6%; Pred. No. 6.8e-22;

Matches 59; Conservative 21; Mismatches 43; Indels 1; Gaps 1;

QY 1 FSVGLTETVTIPNPIRFTKIFYNQNHDSGTGKFCNTPGLYFYFAYHTVYMKOVKVS 60

Db 548 FTVLSKAYPGATVPKFDKLLYNRQHYDPTGIFTCPGLFYFSHVHAKGTNNVWA 607

QY 61 LFKKDKAMLFYDYQENNVQASGVLLHLVGDQVWLQVYGEGERNGLYADNDNSTF 120

Db 608 LYKNGSPVMVYDYORGYLDQASGSAVIDLMENDQVWLQL-PNSESNGLYSSEYVHSSF 666

QY 121 TGFL 124

Db 567 SGFL 670

RESULT 3

CGRUID

collagen alpha 1(X) chain precursor - human

N;Alternate names: procollagen alpha 1(X) chain

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S26396; S30086; S18249; A43901; I51870; S21856

R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.

FEBS Lett. 311, 305-310, 1992

A;Title: Genomic organization and full-length cDNA sequence of human collagen X.

A;Reference number: S26396; MUID:93012005; PMID:1397333

A;Accession: S26396

A;Molecule type: DNA

A;Residues: 1-680 <REI>

A;Cross-references: UNIPROT:Q03692; EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; C
 R;Aprie, S.S. submitted to the EMBL Data Library, March 1992
 A;Reference number: S30085
 A;Accession: S30086
 A;Molecule type: DNA
 A;Residues: 'TTPYGVWVCLL', '52-680' <APT>

A;Cross-references: EMBL:X65120; NID:G23129

A;Note: the initial difference is probably due to translation of an intronic sequence

R;Aprie, S.; Mattai, M.G.; Olsen, B.R.

FEBS Lett. 282, 393-396, 1991

A;Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene to

A;Reference number: S15826; MUID:91243838; PMID:2037056

A;Accession: S15826

A;Molecule type: DNA

A;Residues: 561-647, 'G', '643-666' <AP2>

A;Cross-references: EMBL:X58879; NID:G30013; PIDN:CAA41686.1; PID:G30014

R;Thomas, J.R.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, M.

Biochem. J. 280, 617-623, 1991

A;Title: The human collagen X gene. Complete primary translated sequence and chromosomal

A;Reference number: S18249; MUID:92109659; PMID:1764025

A;Accession: S18249

A;Molecule type: DNA

A;Residues: 1-26, 'T', '28-630' <THO>

A;Cross-references: EMBL:X80392; NID:G30094; PIDN:CAA42933.1; PID:G30095

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Ala

R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.

Dev. Biol. 148, 562-572, 1991

A;Title: In situ hybridization studies on the expression of type X collagen in fetal hume

A;Reference number: A43901; MUID:92077285; PMID:1743401

A;Accession: A43901

A;Molecule type: mRNA

A;Residues: 547-656 <RE2>

A;Cross-references: GB:M74050; GB:D57494; NID:G339884; PIDN:AAA61221.1; PID:G553756

A;Note: sequence extracted from NCBI backbone (NCBI:69012, NCBI:69014)

R;Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.E.

Am. J. Hum. Genet. 54, 169-178, 1994

A;Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain c

pe Schmid.

A;Reference number: I51870; MUID:94136476; PMID:8304336

A;Accession: I51870

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 520-597, 'D', '599-680' <WAL>

A;Cross-references: GB:S80531; NID:G545180; PIDN:AAC0615.1; PID:G545181

A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid

C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C

ed and subsequently O-glycosylated.

C;Genetics:

A;Gene: GDB:COL10A1

A;Cross-references: GDB:128635; OMIM:120110

A;Map position: 6q21-6q22

A;Introns: 52/1

A;Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia

C;Complex: type X collagen may be a homotrimer

C;Function:

A;Description: structural component of extracellular fibrous polymer specifically and tr

be important for skeletogenesis

C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine; t

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-680/Product: collagen alpha 1(X) chain #status predicted <WAT>

F;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>

F;57-519/Region: interrupted helical

F;520-680/Domain: amino-terminal nonhelical #status predicted <NC1>

F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.6%; Score 287.5; DB 1; Length 680;

Best Local Similarity 46.4%; Pred. No. 6.9e-21;

Matches 58; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

```
QY 1 FSVGLETVYVTPNNPIRFTKIFYNQNHVDGSGTGFHCNIPGLYFYHITVMKDVKS 60
Db 554 FTVILSKAYPAIGTPIPFKILYNQHQHDPRTGIFTCCQIPGIYFYSVHVHVKGTWVG 613
QY 61 LFKKDKAMLFYDQYQENNVDOAGSVLLHLEVDGQWLVQVYGEGERNGLYADNDNSTF 120
Db 614 LYKNGTTPVMYTYDEYTKGYLDQAGSAGAIIDLITENDQVWLQL-PNAESNGLYSSEYVHSSF 672
QY 121 TGFLL 125
Db 673 SGFLV 677
RESULT 4
S13301
collagen alpha 1(X) chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C:Accession: S13301
R:Thomas, J. T.; Kwan, A. P. L.; Grant, M. E.; Boot-Handford, R. P.
Biochem. J. 273, 141-148, 1991
A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen.
A:Reference number: S13301; MUID:91113131; PMID:1703407
A:Accession: S13301
A:Molecule type: mRNA
A:Residues: 1-674 <THO>
A:Cross-references: UNIPROT:P23206; EMBL:X53556; NID:G263; PIDN:CAA37624.1; PID:G264
C:Genetics:
A:Gene: COL10A1
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:547-673/Domain: complement C1q carboxyl-terminal homology <CIQ>
Query Match 39.6%; Score 280.5; DB 2; Length 674;
Best Local Similarity 46.4%; Pred. No. 3.5e-20;
Matches 58; Conservative 18; Mismatches 48; Indels 1; Gaps 1;
QY 1 FSVGLETVYVTPNNPIRFTKIFYNQNHVDGSGTGFHCNIPGLYFYHITVMKDVKS 60
Db 548 FTVILSKAYPAIGTPIPFKILYNQHQHDPRTGIFTCKIPGIYFYSVHVHVKGTWVG 607
QY 61 LFKKDKAMLFYDQYQENNVDOAGSVLLHLEVDGQWLVQVYGEGERNGLYADNDNSTF 120
Db 608 LYKNGTTPVMYTYDEYTKGYLDQAGSAGAIIDLITENDQVWLQLPNAES-NGLYSPEYVHSSF 666
QY 121 TGFLL 125
Db 667 SGFLV 671
RESULT 5
S31216
collagen alpha 1(X) chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R:Kong, R. Y. C.; Kwan, K. M.; Lau, E. T.; Thomas, J. T.; Boot-Handford, R. P.; Grant, M. E.;
Eur. J. Biochem. 213, 99-111, 1993
A:Title: Intron-exon structure, alternative use of promoter and expression of the mouse
A:Reference number: S31216; MUID:93238750; PMID:8477738
A:Accession: S31216
A:Molecule type: DNA
A:Residues: 1-680 <KON>
A:Cross-references: UNIPROT:Q05306; EMBL:Z21610; NID:G49793; PIDN:CAA79736.1; PID:G49794
R:Elima, K.; Metsaeranta, M.; Kallio, J.; Peraela, M.; Garofalo, S.; Peraela, M.; de Cro
Biochim. Biophys. Acta 1130, 78-80, 1992
A:Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp
A:Reference number: S28807; MUID:93143676; PMID:8424763
A:Accession: S28807
A:Molecule type: DNA
A:Residues: 1-285, 'A', 287-680 <ELI>
```

```
A:Cross-references: EMBL:X67348; NID:G50480; PIDN:CAA47763.1; PID:G50481
R:Elima, K.; Metsaeranta, M.; Kallio, J.; Peraela, M.; Garofalo, S.; de Cro
Biochim. Biophys. Acta 1130, 78-80, 1992
A:Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN
A:Reference number: S22215; MUID:92182017; PMID:1543751
A:Accession: S22215
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 385-450, 'K', 452-627 <ELA>
A:Cross-references: EMBL:X63013; NID:G49795; PIDN:CAA44741.1; PID:G49796
R:Apfe, S. S.; Olsen, B. R.
Matrix 13, 165-179, 1993
A:Title: Characterization of the mouse type X collagen gene.
A:Reference number: S30127; MUID:92261348; PMID:8492743
A:Accession: S30127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12, 'B', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L',
R:Apfe, S. S.; Seidman, M. F.; Hayashi, M.; Olsen, B. R.
Eur. J. Biochem. 206, 217-224, 1992
A:Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse t
A:Reference number: I48299; MUID:92267014; PMID:1587271
A:Accession: I48299
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'I'
A:Cross-references: EMBL:X65121; NID:G50482; PIDN:CAA46237.1; PID:G667031
R:Summers, T. A.; Irwin, M. H.; Mayne, R.; Ballian, G.
J. Biol. Chem. 263, 581-587, 1988
A:Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody
A:Reference number: S26397; MUID:88087150; PMID:2826450
A:Accession: S26397
A:Molecule type: protein
A:Residues: 'SDGYFSQ', 24-26, 'KQ' <SDM>
C:Genetics:
A:Gene: Coll10a-1
A:Map position: 10
A:Introns: 51/3
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F:553-679/Domain: complement C1q carboxyl-terminal homology <CIQ>
Query Match 39.6%; Score 280.5; DB 2; Length 680;
Best Local Similarity 44.8%; Pred. No. 3.5e-20;
Matches 56; Conservative 20; Mismatches 48; Indels 1; Gaps 1;
QY 1 FSVGLETVYVTPNNPIRFTKIFYNQNHVDGSGTGFHCNIPGLYFYHITVMKDVKS 60
Db 554 FTVILSKAYPAVGAIPPFDEILYNRQHYDPRSGIFTCKIPGIYFYSVHVHVKGTWVG 613
QY 61 LFKKDKAMLFYDQYQENNVDOAGSVLLHLEVDGQWLVQVYGEGERNGLYADNDNSTF 120
Db 614 LYKNGTTPMTYDEYTKGYLDQAGSAGAIIDLITENDQVWLQL-PNAESNGLYSSEYVHSSF 672
QY 121 TGFLL 125
Db 673 SGFLV 677
RESULT 6
S23779
collagen alpha 1(VIII) chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S23779
R:Muraçaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B. R.; Ninomiya, Y.
Eur. J. Biochem. 207, 895-902, 1992
A:Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypepti
A:Reference number: S23779; MUID:92362626; PMID:1499564
A:Accession: S23779
A:Status: preliminary
```

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A:Molecule type: DNA
A:Residues: 1-743 <MUR>
A:Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:G50493; PIDN:CAA47387.1; PID:G13599
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:616-742/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match      38.6%; Score 273.5; DB 1; Length 743;
Best Local Similarity 45.1%; Pred. No. 2e-19;
Matches 55; Conservative 27; Mismatches 35; Indels 5; Gaps 2;

QY 9 VTIP-----NNPIRTKIFVNOQNHVDGSGTKFHCNIPGLYFYAYHITVYMKDKVKSLEKK 64
Db 621 LKVPFPVGPVYKFDKLLNGQNVPQTGFTCEVGVYFYAYHVKGGVWVAFKFN 680

QY 65 DVAKLTQYQYNNVDQASGVLLHLEVDQVWLQVYGEGRNGLYADNDNDSTFTGFL 124
Db 681 NEPMVYTYDEYKGFQDQASGVALLRPGDQVFLQNPPE-QAAGLYAGQYVHSSFSGYL 739

QY 125 LY 126
Db 740 LY 741

RESULT 7
S15435
collagen alpha 1(VIII) chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S15435
R:Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y.
Eur. J. Biochem. 197, 615-622, 1991
A:Title: The complete primary structure of the human alpha-1(VIII) chain and assignment
A:Reference number: S15435; MUID:91231001; PMID:2023894
A:Accession: S15435
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-744 <MUR>
A:Cross-references: UNIPROT:P27658; EMBL:X57527; NID:G30081; PIDN:CAA40748.1; PID:G30082
C:Genetics:
A:Gene: GDB:COL8A1
A:Cross-references: GDB:128104; OMIM:120251
A:Map position: 3q11.1-3q13.2
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F:21-117/Region: amino-terminal nonhelical
F:118-571/Region: interrupted helical
F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match      38.2%; Score 270.5; DB 2; Length 744;
Best Local Similarity 45.5%; Pred. No. 3.9e-19;
Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;

QY 15 PIRTKIFVNOQNHVDGSGTKFHCNIPGLYFYAYHITVYMKDKVKSLEKKAMLTVDQ 74
Db 632 PVKFNKLLNGQNVPQTGFTCEVGVYFYAYHVKGGVWVAFKFNPEVMTYDE 691

QY 75 YOENNVQASGVLLHLEVDQVWLQVYGEGRNGLYADNDNDSTFTGFLY 126
Db 692 YKGFQDQASGVALLRPGDQVFLQNPSE-QAAGLYAGQYVHSSFSGYLLY 742

RESULT 8
A34246
collagen alpha 1(VIII) chain precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A34246
R:Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.
J. Biol. Chem. 264, 16022-16029, 1989
A:Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type
domains similar to those of type X collagen.

A:Molecule type: mRNA
A:Residues: 1-744 <YAM>
A:Cross-references: UNIPROT:P14282; GB:J05042; NID:G164895; PIDN:AAA31204.1; PID:G164896
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F:21-117/Region: amino-terminal nonhelical
F:118-571/Region: interrupted helical
F:572-744/Region: carboxyl-terminal nonhelical
F:617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match      37.8%; Score 267.5; DB 1; Length 744;
Best Local Similarity 45.5%; Pred. No. 7.9e-19;
Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;

QY 15 PIRTKIFVNOQNHVDGSGTKFHCNIPGLYFYAYHITVYMKDKVKSLEKKAMLTVDQ 74
Db 632 PIKFDLLXNGQNVPQTGFTCEVGVYFYAYHVKGGVWVAFKFNPEVMTYDE 691

QY 75 YOENNVQASGVLLHLEVDQVWLQVYGEGRNGLYADNDNDSTFTGFLY 126
Db 692 YKGFQDQASGVALLRPGDQVFLQNPSE-QAAGLYAGQYVHSSFSGYLLY 742

RESULT 9
S23298
collagen alpha 1(VIII) chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S23298
R:Ninomiya, Y.; Castagnola, P.; Gerscke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McCa-
maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pres
A:Title: The molecular biology of collagens with short triple-helical domains.
A:Reference number: S23298
A:Accession: S23298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-744 <NIN>
A:Cross-references: UNIPROT:Q7L2R2
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
F:617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match      37.2%; Score 263.5; DB 1; Length 744;
Best Local Similarity 45.5%; Pred. No. 2e-18;
Matches 51; Conservative 27; Mismatches 33; Indels 1; Gaps 1;

QY 15 PIRTKIFVNOQNHVDGSGTKFHCNIPGLYFYAYHITVYMKDKVKSLEKKAMLTVDQ 74
Db 632 PIKFDLLXNGQNVPQTGFTCEVGVYFYAYHVKGGVWVAFKFNPEVMTYDE 691

QY 75 YOENNVQASGVLLHLEVDQVWLQVYGEGRNGLYADNDNDSTFTGFLY 126
Db 692 YKGFQDQASGVALLRPGDQVFLQNPSE-QAAGLYAGQYVHSSFSGYLLY 742

RESULT 10
B57131
collagen alpha 2(VIII) chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: B57131
R:Muragaki, Y.; Jacenko, O.; Apre, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
J. Biol. Chem. 266, 7721-7727, 1991
A:Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen fami]]
A:Reference number: A57131; MUID:91210292; PMID:2019595
A:Accession: B57131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <MUR>
A:Cross-references: UNIPROT:P25318; GB:M60833
```


Db 122 FTVTRQTHOPPAPNSLIRENAVLNTPQGDYDSTGKFTCKVGLYFVTHAS-HTANLCV 180
QY 60 SLFKKD-KAMLFYDYQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDS 118
Db 181 LLYRSGVKVTFPGHTSKTNQVN--SGVLLRLQVGEVWLAVNDYDMVGI---QGSDS 235
QY 119 TTFGLLLYHD 128
Db 236 VFSGLFLFPD 245

RESULT 14

A55797
collagen precursor, sacculle-specific - bluegill
C:Species: Lepomis macrochirus (bluegill)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 15-Sep-2003
C/Accession: A55797
R: Davis, J.G.; Oberholtzer, J.C.; Burns, F.R.; Greene, M.I.
Science 267, 1031-1034, 1995
A: Title: Molecular cloning and characterization of an inner ear-specific structural protein
A: Reference number: A55797; MUID: 95167486; PMID: 7863331
A: Accession: A55797
A: Status: Preliminary
A: Molecule type: mRNA
A: Residues: 1-423 <DAV>
A: Cross-references: GB: U17431; NID: G687605; PIDN: AAA69978.1; PID: G687606
F: 58-271/Domain: collagenous, triple helix #status predicted <COL>
F: 281-410/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match 30.9%; Score 219; DB 2; Length 423;
Best Local Similarity 43.1%; Pred. No. 3e-14;
Matches 44; Conservative 17; Mismatches 39; Indels 2; Gaps 1;
QY 1 FSVGL--ETVYTPNMPIRFTKIFYNQNVHDGSGKPHCNIPGLYFAYHITVYMKDVK 58
Db 282 FSVGLFPPSRPPPLPVKFKVNGEGHNDPTLNKENVTPGVYLFVSHITVNRPRV 341
QY 59 VSLFKKDKAMLFYDYQYQENNVDAQSGSVLLHLEVGQVWLQ 100
Db 342 AALVNVGVKLRTRDSLYQDIDQASNLALLHLTDGQVWLE 383

RESULT 15

S29328
complement subcomponent C1q chain C - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S29328
R: Petry, F.; Reid, K.B.M.; Loos, M.
Eur. J. Biochem. 209, 129-134, 1992
A: Title: Isolation, sequence analysis and characterization of cDNA clones coding for the
ecerebellin.
A: Reference number: S29328; MUID: 93011118; PMID: 1396691
A: Accession: S29328
A: Status: Preliminary
A: Molecule type: mRNA
A: Residues: 1-246 <PET>
A: Cross-references: UNIPROT: Q02105; EMBL: X66295; NID: G50228; PIDN: CAA46993.1; PID: G50229
C: Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom
F: 122-245/Domain: complement C1q carboxyl-terminal homology <CIQ>

Query Match 29.4%; Score 208.5; DB 2; Length 246;
Best Local Similarity 38.8%; Pred. No. 1.8e-13;
Matches 45; Conservative 23; Mismatches 43; Indels 5; Gaps 3;
QY 13 NMPTRFTKIFYNQNVHDGSGKPHCNIPGLYFAYHITVYMKDVKSLFKDKAMLFY 72
Db 136 NALVRFSNVNTPQGHYNPSTGKFTCEVPGLYFVY--TSHTANLCVHL-NLNLRVASF 193
QY 73 DQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGLLYHD 128
Db 194 CDHMFNSKQVSSGGALLRLRGDEVLSV---NDYNGMGIEGNSVFSGLFLFPD 246

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OM protein - protein search, using sw model

Run on: December 2, 2004, 19:26:59 ; Search time 68 Seconds
(without alignments)
685.806 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708
Sequence: 1 FSVGLTFTVTPNPPIRFTK.....YADNDNSTGTGFLYHDTN 130

Scoring table: BLOSUM62

Gapop 10.0., Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	130	2	AA01485
2	708	100.0	130	7	AD93609
3	708	100.0	137	7	AD93608
4	708	100.0	144	7	AD93607
5	708	100.0	145	7	AD93613
6	708	100.0	157	7	AD93606
7	708	100.0	163	7	AD93612
8	708	100.0	163	7	AD93655
9	708	100.0	187	7	AD93615
10	708	100.0	193	7	AD93614
11	708	100.0	203	7	AD93605
12	708	100.0	226	7	AD93604
13	708	100.0	231	2	AA01480
14	708	100.0	231	4	AB060347
15	708	100.0	233	4	AD93630
16	708	100.0	244	2	AA014807
17	708	100.0	244	3	AA014803
18	708	100.0	244	3	AA014803
19	708	100.0	244	3	AB030233
20	708	100.0	244	4	AB05828
21	708	100.0	244	4	AB05529
22	708	100.0	244	4	AB049598
23	708	100.0	244	4	AB050373
24	708	100.0	244	4	AB049592
25	708	100.0	244	5	AB08223

26	708	100.0	244	5	AAG80254
27	708	100.0	244	6	ABP70915
28	708	100.0	244	6	ABR42035
29	708	100.0	244	6	ABU98378
30	708	100.0	244	6	ABP70905
31	708	100.0	244	6	ABP70905
32	708	100.0	244	6	ABP70905
33	708	100.0	244	6	ABR38000
34	708	100.0	244	6	ABR40088
35	708	100.0	244	6	ABR40249
36	708	100.0	244	6	AA030071
37	708	100.0	244	6	AAE37142
38	708	100.0	244	6	ABR40221
39	708	100.0	244	6	ABR39850
40	708	100.0	244	6	ABR44306
41	708	100.0	244	6	ABP70910
42	708	100.0	244	6	ABP70910
43	708	100.0	244	6	ABR40011
44	708	100.0	244	6	ABR43906
45	708	100.0	244	6	ABU08790
					ABP98485

ALIGNMENTS

RESULT 1
AA01485
ID AA01485 standard; peptide; 130 AA.
XX
AC AA01485;
XX
DT 21-MAY-1999 (first entry)
XX
DE ApM1 protein fragment (residues 115-244).

Dietary lipid; liver; peripheral tissue; medicament; C1q complement;
partitioning; lipolysis stimulated receptor; LSR; hypertension; G1q,R;
obesity; atherosclerosis; insulin resistance; obesity-related disease;
microangiopathy; Type II diabetes; ocular lesion; cachexia;
neoplastic; eating disorder; ApM1.
XX Homo sapiens.
XX
PN WO9907736-A2.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-IB001256.
XX
PR 06-AUG-1997; 97FR-00010088.
XX
PR 22-APR-1998; 98FR-00005032.
XX
PA (GEST) GENSET.
XX
PA (INRM) INSEMI INST NAT SANTE & RECH MEDICALE.
XX
PI Bihaun B, Bougueleret L, Yen-Potin F;
XX
DR WPI; 1999-167364/14.
XX
PT Use of lipolysis stimulated receptor - for developing agents for
modulating partitioning of dietary lipids between the liver and
peripheral tissues, e.g. for treating obesity.
XX
PS Claim 6; Page 70; 77pp; English.
XX
CC The invention relates to agents which influence the partitioning of
dietary lipids between the liver and peripheral tissues for use as
medicament. Sequences shown in AA01481-488 that relate to C1q
complement family and two consensus sequences (AA01499-500) are
potentially useful as such agents. Compounds that influence the
partitioning of dietary lipids between the liver and peripheral tissues
can be used in medicament for treating a condition in which the
partitioning of dietary lipids to the liver is abnormal. A polypeptide

AAG80254 Human APM
ABP70915 APM1 prot
ABR42035 Human APM
ABU98378 Human adi
ABP70905 APM1 prot
ABP70905 APM1 prot
ABP70905 APM1 prot
ABR38000 APM1 poly
ABR40088 APM1 prot
ABR40249 Human APM
AA030071 Human OBG
AAE37142 Human APM
ABR40221 Human gen
ABR39850 APM1 poly
ABR44306 APM1 poly
ABP70910 APM1 prot
ABP70910 APM1 prot
ABR40011 Human aci
ABR43906 APM1 poly
ABU08790 Adiponec
ABP98485 Amino aci

CC having binding specificity for a gamma subunit of the lipolysis
 CC stimulated receptor (LSR) or a GClq.R or GClq.R homologue can be used for
 CC treatment of obesity, where the polypeptide is not a subunit of the LSR.
 CC The agents which increase partitioning of dietary lipids to the liver can
 CC be used for treating obesity-related atherosclerosis, obesity-related
 CC insulin resistance, obesity-related hypertension, microangiopathic lesions
 CC resulting from obesity-related Type II diabetes, ocular lesions caused by
 CC microangiopathy in obese individuals with Type II diabetes, and renal
 CC lesions caused by microangiopathy in obese individuals with Type II
 CC diabetes. Agents which decrease the partitioning of dietary lipids to the
 CC liver can be used for treating cachexia in subjects with neoplastic or
 CC para-neoplastic syndrome or eating disorders. The present sequence
 CC represents a claimed peptide fragment of ApM1
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 708; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.4e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVYTPNMPRTKIFYNQNHVDGSGFKHCNIPGLYFYFAYHITVYMKDVKS 60
 Db 1 FSVGLETVYTPNMPRTKIFYNQNHVDGSGFKHCNIPGLYFYFAYHITVYMKDVKS 60
 Qy 61 LFKKDKAMLFYDQYQENNVQASGVLLHLEVDQVWLVQYGEGERNGLYADNDNSTF 120
 Db 61 LFKKDKAMLFYDQYQENNVQASGVLLHLEVDQVWLVQYGEGERNGLYADNDNSTF 120
 Qy 121 TGFLLYHDTN 130
 Db 121 TGFLLYHDTN 130

RESULT 2
 ADE93609
 ID ADE93609 standard; protein; 130 AA.

XX AC ADE93609;
 XX 12-FEB-2004 (first entry)
 XX Human adiponectin apM1 (115-244) protein.
 DE
 XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 XX antirheumatic; antibacterial; antilipemic; dermatological;
 XX immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 XX atherosclerosis; cardiovascular disease; dyslipidaemia;
 XX rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 XX Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 XX myocardial infarction; inflammation; gene therapy; human; apM1;
 XX wild-type.

XX OS Homo sapiens.
 XX WO2003055916-A2.
 XX 10-JUL-2003.
 XX 20-DEC-2002; 2002WO-DK000897.
 XX 21-DEC-2001; 2001DK-00001952.
 XX 21-DEC-2001; 2001US-0343482P.
 XX 25-APR-2002; 2002DK-00000627.
 XX 25-APR-2002; 2002US-0375492P.
 XX 03-JUL-2002; 2002DK-00001036.
 XX 03-JUL-2002; 2002US-0394117P.
 XX 20-SEP-2002; 2002DK-00001385.
 XX 20-SEP-2002; 2002US-0412169P.
 XX (MAXY-) MAXYGEN APS.
 XX (MAXY-) MAXYGEN HOLDINGS LTD.
 XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;

PI Bogness A;
 XX NPI; 2003-598262/56.
 XX New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX Claim 14; SEQ ID NO 7; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, immunomodulator and anorectic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.

XX Sequence 130 AA;

Query Match 100.0%; Score 708; DB 7; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.4e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLETVYTPNMPRTKIFYNQNHVDGSGFKHCNIPGLYFYFAYHITVYMKDVKS 60
 Db 1 FSVGLETVYTPNMPRTKIFYNQNHVDGSGFKHCNIPGLYFYFAYHITVYMKDVKS 60
 Qy 61 LFKKDKAMLFYDQYQENNVQASGVLLHLEVDQVWLVQYGEGERNGLYADNDNSTF 120
 Db 61 LFKKDKAMLFYDQYQENNVQASGVLLHLEVDQVWLVQYGEGERNGLYADNDNSTF 120
 Qy 121 TGFLLYHDTN 130
 Db 121 TGFLLYHDTN 130

RESULT 3
 ADE93608
 ID ADE93608 standard; protein; 137 AA.

XX AC ADE93608;
 XX 12-FEB-2004 (first entry)
 XX Human adiponectin apM1 (108-244) protein.
 DE
 XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 XX antirheumatic; antibacterial; antilipemic; dermatological;
 XX immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 XX atherosclerosis; cardiovascular disease; dyslipidaemia;
 XX rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 XX Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 XX myocardial infarction; inflammation; gene therapy; human; apM1;
 XX wild-type.
 XX OS Homo sapiens.
 XX WO2003055916-A2.
 XX 10-JUL-2003.
 XX 20-DEC-2002; 2002WO-DK000897.

XX 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX (MAXY-) MAXYGEN APS.
FA (MAXY-) MAXYGEN HOLDINGS LTD.
XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX WPT; 2003-598262/56.
XX New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX Claim 14; SEQ ID NO 6; 184pp; English.
XX The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic, anti-
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipæmic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX Sequence 137 AA;
XX Query Match 100.0%; Score 708; DB 7; Length 137;
XX Best Local Similarity 100.0%; Pred. No. 3.6e-78;
XX Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNHGDSGTGKFCNCIPGLYFYFAYHITVYMKDVKS 60
Db 8 FSVGLETVVTIPNMPIRFTKIFYNQNHGDSGTGKFCNCIPGLYFYFAYHITVYMKDVKS 67
QY 61 LFKDKKAMLFYDQYQENNVQAGSVLLHLEVGQDWLQVYGERNGLYADNDNSTF 120
Db 68 LFKDKKAMLFYDQYQENNVQAGSVLLHLEVGQDWLQVYGERNGLYADNDNSTF 127
QY 121 TGFLLYHDTN 130
Db 128 TGFLLYHDTN 137
RESULT 4
ADE93607
ID ADE93607 standard; protein; 144 AA.
XX ADE93607;
AC ADE93607;
XX 12-FEB-2004 (first entry)
DT Human adiponectin apM1(101-244) protein.
XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipæmic; dermatological;

KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
KW wild-type.
XX Homo sapiens.
OS WO2003055916-A2.
XX 10-JUL-2003.
XX 20-DEC-2002; 2002WO-DK000897.
XX 21-DEC-2001; 2001DK-00001952.
PR 21-DEC-2001; 2001US-0343482P.
PR 25-APR-2002; 2002DK-00000627.
PR 25-APR-2002; 2002US-0375492P.
PR 03-JUL-2002; 2002DK-00001036.
PR 03-JUL-2002; 2002US-0394117P.
PR 20-SEP-2002; 2002DK-00001385.
PR 20-SEP-2002; 2002US-0412169P.
XX (MAXY-) MAXYGEN APS.
FA (MAXY-) MAXYGEN HOLDINGS LTD.
XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogsnes A;
XX WPT; 2003-598262/56.
XX New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX Claim 44; SEQ ID NO 5; 184pp; English.
XX The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic, anti-
CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipæmic,
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX Sequence 144 AA;
XX Query Match 100.0%; Score 708; DB 7; Length 144;
XX Best Local Similarity 100.0%; Pred. No. 3.9e-78;
XX Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVVTIPNMPIRFTKIFYNQNHGDSGTGKFCNCIPGLYFYFAYHITVYMKDVKS 60
Db 15 FSVGLETVVTIPNMPIRFTKIFYNQNHGDSGTGKFCNCIPGLYFYFAYHITVYMKDVKS 74
QY 61 LFKDKKAMLFYDQYQENNVQAGSVLLHLEVGQDWLQVYGERNGLYADNDNSTF 120
Db 75 LFKDKKAMLFYDQYQENNVQAGSVLLHLEVGQDWLQVYGERNGLYADNDNSTF 134
QY 121 TGFLLYHDTN 130
Db 135 TGFLLYHDTN 144

RESULT 5
ADE93613
ID ADE93613 standard; protein; 145 AA.
XX
AC ADE93613;
XX
DE 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(100-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
XX
PR 21-DEC-2001; 2001US-0343482P.
XX
PR 25-APR-2002; 2002DK-00000627.
XX
PR 25-APR-2002; 2002US-0375492P.
XX
PR 03-JUL-2002; 2002DK-00001036.
XX
PR 03-JUL-2002; 2002US-0394117P.
XX
PR 20-SEP-2002; 2002DK-00001385.
XX
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogness A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 11; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic, anti-
CC antidiabetic, cardiant, antirheumatic, immunomodulator and anorectic
CC dermatological, immunosuppressive, immunomodulator and anorectic
CC activities and may be useful for treating diabetes, obesity,
CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
CC infarction and destructive processes related to activation of the
CC inflammatory system, as well as during gene therapy procedures. The
CC current sequence is that of the human adiponectin apM1 protein of the
CC invention.
XX
SQ Sequence 145 AA;
Query Match 100.0%; Score 708; DB 7; Length 145;

Best Local Similarity 100.0%; Pred. No. 3.9e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVVTPNNPIRFTKIFYNQNNHYDGTGKFKHCNIPGLYYPAYHITVYMKDKVKS 60
XX
DB 16 FSVGLETVVTPNNPIRFTKIFYNQNNHYDGTGKFKHCNIPGLYYPAYHITVYMKDKVKS 75
XX
QY 61 LFKKDKAMLFYDQYQENNVQASGVLHLEVDQVWLVQVYGERNGLYADNDNSTF 120
DB 76 LFKKDKAMLFYDQYQENNVQASGVLHLEVDQVWLVQVYGERNGLYADNDNSTF 135
XX
QY 121 TGFLLYHDTN 130
DB 136 TGFLLYHDTN 145
XX
RESULT 6
ADE93606
ID ADE93606 standard; protein; 157 AA.
XX
AC ADE93606;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1(88-244) protein.
XX
KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
KW antirheumatic; antibacterial; antilipemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1;
wild-type.
XX
OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-DK000897.
XX
PR 21-DEC-2001; 2001DK-00001952.
XX
PR 21-DEC-2001; 2001US-0343482P.
XX
PR 25-APR-2002; 2002DK-00000627.
XX
PR 25-APR-2002; 2002US-0375492P.
XX
PR 03-JUL-2002; 2002DK-00001036.
XX
PR 03-JUL-2002; 2002US-0394117P.
XX
PR 20-SEP-2002; 2002DK-00001385.
XX
PR 20-SEP-2002; 2002US-0412169P.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
PI Bogness A;
XX
DR WPI; 2003-598262/56.
XX
PT New conjugate comprising an adiponectin polypeptide and a first non-
PT polypeptide moiety, useful for preparing a composition for treating a
PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
XX
PS Claim 44; SEQ ID NO 4; 184pp; English.
XX
CC The invention relates to a novel conjugate comprising an adiponectin
CC polypeptide and a first non-polypeptide moiety covalently attached to the
CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
CC acid residue having an attachment group for the first non-polypeptide
CC moiety which has been introduced in a position where the parent
CC adiponectin is occupied by a surface exposed amino acid residue. The
CC conjugate of the invention demonstrates antiarteriosclerotic,
XX

CC anti-diabetic, cardiant, antirheumatic, antibacterial, antilipaeamic, antilipaeamic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.

XX SQ Sequence 157 AA;
 Query Match 100.0%; Score 708; DB 7; Length 157;
 Best Local Similarity 100.0%; Pred. No. 4.4e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVYVTPNPIRFTKIFYNQNHVDGSGKFCNIPGLYFYFAYHITVYMKDVKS 60
 DB 28 FSVGLETVYVTPNPIRFTKIFYNQNHVDGSGKFCNIPGLYFYFAYHITVYMKDVKS 87
 QY 61 LFKDKAMLFYDQYQENNVDOAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
 DB 88 LFKDKAMLFYDQYQENNVDOAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 147
 QY 121 TGFLLYHDTN 130
 DB 148 TGFLLYHDTN 157

RESULT 7
 ADE93612
 ID ADE93612 standard; protein; 163 AA.
 XX AC ADE93612;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human adiponectin apM1 (82-244) protein.
 XX KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antirheumatic; antibacterial; antilipaeamic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1;
 KW wild-type.
 XX OS Homo sapiens.
 XX FN WO2003055916-A2.
 XX PD 10-JUL-2003.
 XX PF 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 XX PR 21-DEC-2001; 2001US-0343482P.
 XX PR 25-APR-2002; 2002DK-00000627.
 XX PR 03-JUL-2002; 2002US-0375492P.
 XX PR 03-JUL-2002; 2002DK-00001036.
 XX PR 03-JUL-2002; 2002US-0394117P.
 XX PR 20-SEP-2002; 2002DK-00001385.
 XX PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bognes A;
 XX WPI; 2003-598262/56.

DR N-PSDB; ADE93618.
 XX New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX Claim 44; SEQ ID NO 10; 184pp; English.
 XX The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaeamic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.

XX SQ Sequence 163 AA;
 Query Match 100.0%; Score 708; DB 7; Length 163;
 Best Local Similarity 100.0%; Pred. No. 4.6e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVYVTPNPIRFTKIFYNQNHVDGSGKFCNIPGLYFYFAYHITVYMKDVKS 60
 DB 34 FSVGLETVYVTPNPIRFTKIFYNQNHVDGSGKFCNIPGLYFYFAYHITVYMKDVKS 93
 QY 61 LFKDKAMLFYDQYQENNVDOAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
 DB 94 LFKDKAMLFYDQYQENNVDOAGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 153
 QY 121 TGFLLYHDTN 130
 DB 154 TGFLLYHDTN 163

RESULT 8
 ADE93655
 ID ADE93655 standard; protein; 163 AA.
 XX AC ADE93655;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human adiponectin Y11N-apM1 (92-244) mutant protein.
 XX KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antirheumatic; antibacterial; antilipaeamic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1; mutant;
 KW mutein.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX FN WO2003055916-A2.
 XX PD 10-JUL-2003.
 XX PF 20-DEC-2002; 2002WO-DK000897.

PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogsnes A;
 XX
 DR WPI; 2003-598262/56.
 DR N-PSDB; ADE93667.
 XX
 PT New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX
 PS Claim 38; SEQ ID NO 53; 184pp; English.
 XX
 CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaeamic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1(82-244) mutant
 CC protein of the invention.
 XX
 SQ Sequence 163 AA;
 Query Match 100.0%; Score 708; DB 7; Length 163;
 Best Local Similarity 100.0%; Pred. No. 4.6e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSVGLTYYTIPNMPFIRTKIFYNQNHGDSGTGKFCNIPGLYFYFAYHITVYMKDVKS 60
 DB 34 FSVGLTYYTIPNMPFIRTKIFYNQNHGDSGTGKFCNIPGLYFYFAYHITVYMKDVKS 93
 QY 61 LFKKDKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGERNGLYADNDNSTF 120
 DB 94 LFKKDKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGERNGLYADNDNSTF 153
 QY 121 TGFLLYHDTN 130
 DB 154 TGFLLYHDTN 163
 RESULT 9
 ADE93615
 ID ADE93615 standard; protein; 187 AA.
 XX
 AC ADE93615;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human adiponectin apM1(58-244) protein.
 XX
 KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antirheumatic; antibacterial; antilipaeamic; dermatological;

KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1;
 wild-type.
 XX
 OS Homo sapiens.
 XX
 PN WO2003055916-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 20-DEC-2002; 2002WO-DK000897.
 XX
 PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogsnes A;
 XX
 DR WPI; 2003-598262/56.
 DR N-PSDB; ADE93617.
 XX
 PT New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX
 PS Claim 44; SEQ ID NO 13; 184pp; English.
 XX
 CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipaeamic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.
 XX
 SQ Sequence 187 AA;
 Query Match 100.0%; Score 708; DB 7; Length 187;
 Best Local Similarity 100.0%; Pred. No. 5.5e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSVGLTYYTIPNMPFIRTKIFYNQNHGDSGTGKFCNIPGLYFYFAYHITVYMKDVKS 60
 DB 58 FSVGLTYYTIPNMPFIRTKIFYNQNHGDSGTGKFCNIPGLYFYFAYHITVYMKDVKS 117
 QY 61 LFKKDKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGERNGLYADNDNSTF 120
 DB 118 LFKKDKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGERNGLYADNDNSTF 177
 QY 121 TGFLLYHDTN 130
 |||||

Db 178 TGFLYHDTN 187

RESULT 10

AD93614

ID ADE93614 standard; protein; 193 AA.

XX

AC ADE93614;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human adiponectin apM1 (52-244) protein.

XX

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;

XX anti-rheumatic; antibacterial; antilipaeamic; dermatological;

XX immunosuppressive; immunomodulator; anorectic; diabetes; obesity;

XX atherosclerosis; cardiovascular disease; dyslipidaemia;

KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;

KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;

KW myocardial infarction; inflammation; gene therapy; human; apM1;

XX wild-type.

OS Homo sapiens.

XX

XX WO2003055916-A2.

FN

XX 10-JUL-2003.

XX

XX 20-DEC-2002; 2002WO-DK000897.

XX

XX 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-00001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

XX (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;

PI Bognes A;

XX

XX WPI; 2003-598262/56.

DR N-PSDB; ADE93616.

XX

XX New conjugate comprising an adiponectin polypeptide and a first non-

PT polypeptide moiety, useful for preparing a composition for treating a

PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX

XX Claim 44; SEQ ID NO 12; 184pp; English.

PS

XX The invention relates to a novel conjugate comprising an adiponectin

CC polypeptide and a first non-polypeptide moiety covalently attached to the

CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino

CC acid residue having an attachment group for the first non-polypeptide

CC moiety which has been introduced in a position where the parent

CC adiponectin is occupied by a surface exposed amino acid residue. The

CC conjugate of the invention demonstrates antiarteriosclerotic,

CC antidiabetic, cardiant, anti-rheumatic, antibacterial, antilipaeamic,

CC dermatological, immunosuppressive, immunomodulator and anorectic

CC activities and may be useful for treating diabetes, obesity,

CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid

CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren

CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial

CC infarction and destructive processes related to activation of the

CC inflammatory system, as well as during gene therapy procedures. The

CC current sequence is that of the human adiponectin apM1 protein of the

CC invention.

XX

XX Sequence 193 AA;

SQ

Query Match 100.0%; Score 708; DB 7; Length 193;

Best Local Similarity 100.0%; Pred. No. 5.8e-78;

Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVTTPNMPIRTKIFYNQNHVDGSGTKFHCNIGLYYFAYHITVYMKDVKS 60

DB 64 FSVGLETVTTPNMPIRTKIFYNQNHVDGSGTKFHCNIGLYYFAYHITVYMKDVKS 123

QY 61 LFKDKAMLFTYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120

DB 124 LFKDKAMLFTYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 183

QY 121 TGFLYHDTN 130

DB 184 TGFLYHDTN 193

RESULT 11

AD93605

ID ADE93605 standard; protein; 203 AA.

XX

AC ADE93605;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human adiponectin apM1 (42-244) protein.

XX

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;

KW anti-rheumatic; antibacterial; antilipaeamic; dermatological;

KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;

KW atherosclerosis; cardiovascular disease; dyslipidaemia;

KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;

KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;

KW myocardial infarction; inflammation; gene therapy; human; apM1;

XX wild-type.

OS Homo sapiens.

XX

XX WO2003055916-A2.

FN

XX 10-JUL-2003.

XX

XX 20-DEC-2002; 2002WO-DK000897.

XX

XX 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-00001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

XX (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;

PI Bognes A;

XX

XX WPI; 2003-598262/56.

DR

XX New conjugate comprising an adiponectin polypeptide and a first non-

PT polypeptide moiety, useful for preparing a composition for treating a

PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX

XX Claim 44; SEQ ID NO 3; 184pp; English.

PS

XX The invention relates to a novel conjugate comprising an adiponectin

CC polypeptide and a first non-polypeptide moiety covalently attached to the

CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino

CC acid residue having an attachment group for the first non-polypeptide

CC moiety which has been introduced in a position where the parent

CC adiponectin is occupied by a surface exposed amino acid residue. The

CC conjugate of the invention demonstrates antiarteriosclerotic,

CC antidiabetic, cardiant, anti-rheumatic, antibacterial, antilipaeamic,

CC dermatological, immunosuppressive, immunomodulator and anorectic

CC activities and may be useful for treating diabetes, obesity,

CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid

CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren

CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial

CC infarction and destructive processes related to activation of the

CC inflammatory system, as well as during gene therapy procedures. The

CC current sequence is that of the human adiponectin apM1 protein of the

CC invention.

XX

XX Sequence 193 AA;

SQ

CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic.
 CC anti-diabetic, cardiant, anti-rheumatic, antibacterial, anti-lipidemic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.

XX Sequence 203 AA;

Query Match 100.0%; Score 708; DB 7; Length 203;
 Best Local Similarity 100.0%; Pred. No. 6,2e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETYVTIPNMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 60
 DB 74 FSVGLETYVTIPNMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 133
 QY 61 LFKKDKXAMLFYDQYQENNVDOASGSVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 120
 DB 134 LFKKDKXAMLFYDQYQENNVDOASGSVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 193
 QY 121 TGFLLYHDTN 130
 DB 194 TGFLLYHDTN 203

RESULT 12

AD93604
 ID ADE93604 standard; protein; 226 AA.

AC ADE93604;

DT 12-FEB-2004 (first entry)

DE Human adiponectin apM1 (19-244) protein.

KW adiponectin conjugate; antiarteriosclerotic; anti-diabetic; cardiant;
 KW anti-rheumatic; antibacterial; anti-lipidemic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1;
 KW wild-type.

OS Homo sapiens.

PN WO2003055916-A2.

PD 10-JUL-2003.

PF 20-DEC-2002; 2002WO-DK000897.

PR 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-00001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogsgnes A;

XX

DR WPI; 2003-598262/56.

XX New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX Claim 14; SEQ ID NO 2; 184pp; English.

CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC anti-diabetic, cardiant, anti-rheumatic, antibacterial, anti-lipidemic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 protein of the
 CC invention.

XX Sequence 226 AA;

Query Match 100.0%; Score 708; DB 7; Length 226;
 Best Local Similarity 100.0%; Pred. No. 7,2e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETYVTIPNMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 60
 DB 97 FSVGLETYVTIPNMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 156
 QY 61 LFKKDKXAMLFYDQYQENNVDOASGSVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 120
 DB 157 LFKKDKXAMLFYDQYQENNVDOASGSVLLHLEVGQVWLVQVYGEGERNGLYADNDSTF 216
 QY 121 TGFLLYHDTN 130
 DB 217 TGFLLYHDTN 226

RESULT 13

AA21808
 ID AAY21808 standard; protein; 231 AA.

XX AAY21808;

DT 10-SEP-1999 (first entry)

DE Adipose most abundant gene transcription product 1 (apM1) fragment.

KW Smooth muscle proliferation; secretion factor; apM1; adipose;

KW adipose most abundant gene transcription product 1; obesity;

KW arteriosclerosis; restenosis; angina pectoris; myocardial infarction.

XX Unidentified.

XX WO9921577-A1.

XX 06-MAY-1999.

XX 27-OCT-1998; 98WO-JP004862.

XX 29-OCT-1997; 97JP-00297569.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Matsuzawa Y, Ohmoto Y;

XX WPI; 1999-418412/35.
XX Inhibition of smooth muscle proliferation using secretion factor apM1.
XX Example; Page 59-60; 65pp; Japanese.
XX Then invention relates to the inhibition of smooth muscle proliferation
CC using a composition containing secretion factor apM1 (adipose most
CC abundant gene transcript product 1), together with a suitable carrier.
CC apM1 is expressed specifically in adipose tissue and the composition is
CC used for the prevention and treatment of arteriosclerosis; restenosis
CC following vascular reconstruction; and treatment and diagnosis of
CC diseases related to obesity, and disorders associated with it such as
CC angina pectoris and myocardial infarction. The present sequence
CC represents a fragment of apM1 isolated from abdominal fat tissue of myoma
CC uteri
XX
SQ Sequence 231 AA;
Query Match 100.0%; Score 708; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYTIPIPNPIRFTKIFYNQNHVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 60
DB 102 FSVGLETVYTIPIPNPIRFTKIFYNQNHVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 161
QY 61 LFKKDKAMLFYDQYQENNVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 120
DB 162 LFKKDKAMLFYDQYQENNVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 221
QY 121 TGFLLYHDTN 130
DB 222 TGFLLYHDTN 231
RESULT 14
AAB60347
ID AAB60347 standard; protein; 231 AA.
AC AAB60347;
DT 06-APR-2001 (first entry)
XX Recombinant human apM1 protein (residues 15-244 + Met1), SEQ ID NO:3.
XX Antigenic protein detection; sodium sulphate; ELISA;
KW enzyme-linked immunosorbent assay; human apM1; recombinant expression;
KW Escherichia coli; adipose most abundant gene transcript 1;
KW adipose-specific collagen-like factor.
XX Homo sapiens.
OS Synthetic.
XX JP2000304748-A.
PN
XX
XX 02-NOV-2000.
XX 21-APR-1999; 99JP-00114170.
PF
XX 21-APR-1999; 99JP-00114170.
PR
XX (SAKA) OTSUKA PHARM CO LTD.
PA
XX WPI; 2001-127687/14.
DR
XX Detection of an antigenic protein comprises use of enzyme linked
PT immunosorbant assay.
XX
XX Example 1; Page 7-8; 10pp; Japanese.
PS
XX The invention relates to a method for detecting an antigenic protein. The

CC method comprises boiling the sample containing the antigenic protein in
CC the presence of sodium sulphate, diluting it in buffer, and detecting the
CC enzyme by enzyme-linked immunosorbent assay (ELISA). In an
CC exemplification of the invention, residues 15-244 (plus an initial Met
CC residue) of human apM1 (adipose most abundant gene transcript 1;
CC AAB60347), an adipose-specific collagen-like factor, was recombinantly
CC expressed in Escherichia coli. Using the method of the invention, it was
CC found that apM1 was expressed mainly in the inclusion body fragment as an
CC approximately 30 kd protein. The present sequence represents the
CC recombinantly expressed human apM1
XX
SQ Sequence 231 AA;
Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.4e-78;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYTIPIPNPIRFTKIFYNQNHVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 60
DB 102 FSVGLETVYTIPIPNPIRFTKIFYNQNHVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 161
QY 61 LFKKDKAMLFYDQYQENNVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 120
DB 162 LFKKDKAMLFYDQYQENNVDSGSGVLLHLEVDQVWLQVYGEGERNGLYADNDNSTF 221
QY 121 TGFLLYHDTN 130
DB 222 TGFLLYHDTN 231
RESULT 15
ADD93530
ID ADD93530 standard; protein; 233 AA.
XX
XX AC ADD93530;
XX 29-JAN-2004 (first entry)
DT
XX Novel NOV2e, homologous to human adiponectin.
DE
XX NOV2e; human; adiponectin; gene therapy.
KW
XX Homo sapiens.
OS
XX WC2003078572-A2.
PN
XX 25-SEP-2003.
PD
XX 06-MAR-2003; 2003WO-US006859.
PF
XX 15-MAR-2002; 2002US-0365034P.
PR
XX 19-MAR-2002; 2002US-0365477P.
PR
XX 21-MAR-2002; 2002US-0366420P.
PR
XX 05-MAR-2003; 2003US-00379747.
PR
XX (CURA-) CURAGEN CORP.
PA
XX Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Gangolli EA;
XX Malyankar UM, Miller CE, Cui CE, Ort T, Patturajan M, Rastelli L;
PI Rieger DK, Shimkets RA, Zernhusen BD;
PI
XX WPI; 2003-779122/73.
DR
XX N-PSDB; ADD93529.
DR
XX New isolated NOVX polypeptides and polynucleotides, useful for
XX preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, parkinson's disease,
PT asthma, or infections.
XX
XX Claim 1; Page 108; 205pp; English.
PS
XX The present sequence is the protein sequence of a novel polypeptide,
CC designated NOV2e, that shows amino acid sequence homology to the human

CC adiponectin (adipose most abundant gene transcript 1, APM1). The
 CC adiponectin gene is the most abundant gene transcript in adipose cells
 CC that regulates lipid metabolism. An interaction between adiponectin and
 CC calcium modulating ligand was identified, indicating a novel pathway by
 CC which adiponectin may induce lipid breakdown in muscle cells and
 CC adipocytes. The invention is based on the identification of proteins and
 CC polypeptides, and the nucleic acids encoding them, that are
 CC differentially modulated in a pathological state, disease or an abnormal
 CC condition or state. These are targets for therapeutic agents and can be
 CC used in screening methodologies to identify candidate therapeutic agents
 CC which interact with the target and thereby exert a desired or favourable
 CC effect, e.g. in neurogenesis, cell differentiation, cell proliferation,
 CC haematopoiesis, wound healing and angiogenesis. Methods for diagnosis,
 CC treatment and prevention of disorders involving the novel human nucleic
 CC acids and proteins are provided. The polypeptides are also used to raise
 CC antibodies, useful in therapy and diagnosis.

XX ^
 SQ Sequence 233 AA;

Query Match 100.0%; Score 708; DB 7; Length 233;
 Best Local Similarity 100.0%; Pred. No. 7.5e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	FSVGLTYVTIPNMP	IRFTKIFYNQ	QNHVDG	STGK	PHCNIPGL	YFYFAYHITVYMKDKVVS	60
Db	104	FSVGLTYVTIPNMP	IRFTKIFYNQ	QNHVDG	STGK	PHCNIPGL	YFYFAYHITVYMKDKVVS	163
QY	61	LPKDKXAMLFYDQ	YQENNVDA	SGSVLLH	LEVGDQ	WLVQY	YGEGERNGLYADNDNSTF	120
Db	164	LPKDKXAMLFYDQ	YQENNVDA	SGSVLLH	LEVGDQ	WLVQY	YGEGERNGLYADNDNSTF	223
QY	121	TGFLLYHDTN	130					
Db	224	TGFLLYHDTN	233					

Search completed: December 2, 2004, 19:33:35
 Job time : 71 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 19:32:25 ; Search time 144 Seconds

(without alignments)
321.951 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708

Sequence: 1 FSVGLTYVTIENPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708	100.0	130	13	US-10-072-159-11
2	708	100.0	130	13	Sequence 11, Appl
3	708	100.0	130	13	Sequence 11, Appl
4	708	100.0	137	14	US-10-325-717-7
5	708	100.0	144	14	US-10-325-717-6
6	708	100.0	145	14	US-10-325-717-5
7	708	100.0	157	14	US-10-325-717-11
8	708	100.0	163	14	US-10-325-717-4
9	708	100.0	163	14	US-10-325-717-10
10	708	100.0	187	14	US-10-325-717-53
11	708	100.0	187	14	US-10-325-717-13
12	708	100.0	193	14	US-10-325-717-12
13	708	100.0	203	14	US-10-325-717-3
13	708	100.0	226	14	US-10-325-717-2

14	708	100.0	231	14	US-10-189-493-2	Sequence 2, Appl
15	708	100.0	233	15	US-10-379-747-14	Sequence 14, Appl
16	708	100.0	244	9	US-09-776-976-6	Sequence 6, Appl
17	708	100.0	244	9	US-09-758-055-6	Sequence 6, Appl
18	708	100.0	244	9	US-09-909-547-6	Sequence 6, Appl
19	708	100.0	244	9	US-09-911-176B-48	Sequence 48, Appl
20	708	100.0	244	14	US-10-180-762-51	Sequence 51, Appl
21	708	100.0	244	14	US-10-231-814-6	Sequence 6, Appl
22	708	100.0	244	14	US-10-234-000-4	Sequence 4, Appl
23	708	100.0	244	14	US-10-360-186-51	Sequence 51, Appl
24	708	100.0	244	14	US-10-321-164-3	Sequence 3, Appl
25	708	100.0	244	14	US-10-376-460-6	Sequence 6, Appl
26	708	100.0	244	14	US-10-189-493-1	Sequence 1, Appl
27	708	100.0	244	14	US-10-197-293-3	Sequence 3, Appl
28	708	100.0	244	14	US-10-325-717-1	Sequence 1, Appl
29	708	100.0	244	14	US-10-411-120-67	Sequence 67, Appl
30	708	100.0	244	15	US-10-379-747-6	Sequence 6, Appl
31	708	100.0	244	15	US-10-379-747-8	Sequence 8, Appl
32	708	100.0	244	15	US-10-379-747-10	Sequence 10, Appl
33	708	100.0	244	15	US-10-621-787-3	Sequence 3, Appl
34	708	100.0	244	15	US-10-285-833-6	Sequence 6, Appl
35	708	100.0	250	15	US-10-379-747-12	Sequence 12, Appl
36	703	99.3	145	14	US-10-325-717-27	Sequence 27, Appl
37	703	99.3	163	14	US-10-325-717-18	Sequence 18, Appl
38	703	99.3	163	14	US-10-325-717-55	Sequence 55, Appl
39	703	99.3	163	14	US-10-325-717-60	Sequence 60, Appl
40	703	99.3	187	14	US-10-325-717-33	Sequence 33, Appl
41	703	99.3	193	14	US-10-325-717-30	Sequence 30, Appl
42	703	99.3	203	14	US-10-325-717-21	Sequence 21, Appl
43	702	99.2	144	14	US-10-325-717-25	Sequence 25, Appl
44	702	99.2	145	14	US-10-325-717-26	Sequence 26, Appl
45	702	99.2	145	14	US-10-325-717-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-10-072-159-11
; Sequence 11, Application US/10072159
; Publication No. US20020151498A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET-036APC
; CURRENT APPLICATION NUMBER: US/10/072,159
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/485,316
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRI
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-10-072-159-11

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity. 100.0%; Pred. No. 6.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGLTYVTIENPIRFTKIFYNQNHVDGSGTKPHCNIPGLYFAVHITVYMKDKVYS 60

Db 1 FSVGLETVYTIPIPNMIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
QY 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 2

US-10-060-845-11
; Sequence 11, Application US/10060845
; Publication No. US20020165154A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET.038APC
; CURRENT APPLICATION NUMBER: US/10/060,845
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: U.S. 09/485,316
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10098
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT 1998/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-10-060-845-11

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 6.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYTIPIPNMIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
Db 1 FSVGLETVYTIPIPNMIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
QY 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 3

US-10-325-717-7
; Sequence 7, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610

; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1 (115-244)
US-10-325-717-7

Query Match 100.0%; Score 708; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 6.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FSVGLETVYTIPIPNMIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
Db 1 FSVGLETVYTIPIPNMIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
QY 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 4

US-10-325-717-6
; Sequence 6, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1 (108-244)
US-10-325-717-6

Query Match 100.0%; Score 708; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 6.6e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Query Match      100.0%; Score 708; DB 14; Length 157;
Best Local Similarity 100.0%; Pred. No. 7.8e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 60
Db 28 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 87
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 88 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 147
QY 121 TGFLLYHDTN 130
Db 148 TGFLLYHDTN 157
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RESULT 8

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US-10-325-717-10
; Sequence 10, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apm1(82-244)
US-10-325-717-10
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Query Match      100.0%; Score 708; DB 14; Length 163;
Best Local Similarity 100.0%; Pred. No. 8.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 60
Db 34 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 93
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 94 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 153
QY 121 TGFLLYHDTN 130
Db 154 TGFLLYHDTN 163
```

RESULT 9

```
US-10-325-717-53
; Sequence 53, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct Y11N-apm1(82-244)
US-10-325-717-53
```

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Query Match      100.0%; Score 708; DB 14; Length 163;
Best Local Similarity 100.0%; Pred. No. 8.2e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 60
Db 34 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 93
QY 61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 120
Db 94 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNDSTF 153
QY 121 TGFLLYHDTN 130
Db 154 TGFLLYHDTN 163
```

RESULT 10

```
US-10-325-717-13
; Sequence 13, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 187
; TYPE: PRT
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```
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(58-244)
US-10-325-717-13

Query Match      100.0%; Score 708; DB 14; Length 187;
Best Local Similarity 100.0%; Pred. No. 9.7e-70; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0;

QY 1 FSVGLETVTTPNPIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
DB 58 FSVGLETVTTPNPIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 117
QY 61 LFKDKKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
DB 118 LFKDKKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 177
QY 121 TGFLLYHDTN 130
DB 178 TGFLLYHDTN 187

RESULT 11
US-10-325-717-12
; Sequence 12, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(52-244)
US-10-325-717-12

Query Match      100.0%; Score 708; DB 14; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e-69; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0;

QY 1 FSVGLETVTTPNPIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
DB 64 FSVGLETVTTPNPIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 123
QY 61 LFKDKKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
DB 124 LFKDKKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 183
QY 121 TGFLLYHDTN 130
DB 184 TGFLLYHDTN 193

RESULT 12
```

```
US-10-325-717-3
; Sequence 3, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(42-244)
US-10-325-717-3

Query Match      100.0%; Score 708; DB 14; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.1e-69; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0;

QY 1 FSVGLETVTTPNPIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 60
DB 74 FSVGLETVTTPNPIRFTKIFYNQNHVDGSGTKFHCNIPGLYFYFAYHITVYMKDVKS 133
QY 61 LFKDKKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
DB 134 LFKDKKAMLFYDQYQENNVDQASGVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 193
QY 121 TGFLLYHDTN 130
DB 194 TGFLLYHDTN 203

RESULT 13
US-10-325-717-2
; Sequence 2, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apML(19-244)
US-10-325-717-2
```

```
Query Match      100.0%; Score 708; DB 14; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.2e-69;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGTKFHCNIPGLYYFAYHITVYMKDKVKS 60
Db      97 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGTKFHCNIPGLYYFAYHITVYMKDKVKS 156

QY      61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
Db      157 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 216

QY      121 TGFLLYHDTN 130
Db      217 TGFLLYHDTN 226
```

```
RESULT 14
US-10-189-493-2
; Sequence 2, Application US/10189493
; Publication No. US20030166551A1
; GENERAL INFORMATION:
; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
; TITLE OF INVENTION: therefor
; FILE REFERENCE: P98-51
; CURRENT APPLICATION NUMBER: US/10/189,493
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US/09/530,423
; FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Abdominal fat tissue from myoma uteri
US-10-189-493-2
```

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Query Match      100.0%; Score 708; DB 14; Length 231;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGTKFHCNIPGLYYFAYHITVYMKDKVKS 60
Db      102 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGTKFHCNIPGLYYFAYHITVYMKDKVKS 161

QY      61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
Db      162 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 221

QY      121 TGFLLYHDTN 130
Db      222 TGFLLYHDTN 231
```

```
RESULT 15
US-10-379-747-14
; Sequence 14, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Chant, John S.;
; APPLICANT: Chaudhuri, Amitabha ;
```

```
; APPLICANT: Edinger, Shlomit R.;
; APPLICANT: Gangolli, Esha A.;
; APPLICANT: Malvankar, Uriel M.;
; APPLICANT: Miller, Charles E.;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Ort, Tatiana A.;
; APPLICANT: Patturajan, Meera ;
; APPLICANT: Rastelli, Luca ;
; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THEAPRUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-368B
; CURRENT APPLICATION NUMBER: US/10/379,747
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/365,034
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/366,420
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/365,477
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 14
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-747-14
```

```
Query Match      100.0%; Score 708; DB 15; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGTKFHCNIPGLYYFAYHITVYMKDKVKS 60
Db      104 FSVGLETVYTIENMPIRFTKIFYNQNHVDGSGTKFHCNIPGLYYFAYHITVYMKDKVKS 163

QY      61 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 120
Db      164 LFKKDKAMLFYDQYQENNVDAQSGSVLLHLEVGQVWLQVYGEGERNGLYADNDNSTF 223

QY      121 TGFLLYHDTN 130
Db      224 TGFLLYHDTN 233
```

Search completed: December 2, 2004, 19:38:04
Job time : 145 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2004, 09:18:03 ; Search time 399 Seconds
(without alignments)
1710.338 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLEYTYIENMIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DSV=xlp
-Q=/cgn2_1/USPTO.spool_P/US10072159/runat_02122004_142304_15552/app_query.fasta_1.327
-DB=N Geneseg 23Sep04 -QFW=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFW=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10072159 @CGN 1 1 708 @runat_02122004_142304_15552 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseg 23Sep04.*

- 1: genesegn1980s.*
- 2: genesegn1990s.*
- 3: genesegn2000s.*
- 4: genesegn2001as.*
- 5: genesegn2001bs.*
- 6: genesegn2002as.*
- 7: genesegn2002bs.*
- 8: genesegn2003as.*
- 9: genesegn2003bs.*
- 10: genesegn2003cs.*
- 11: genesegn2003ds.*
- 12: genesegn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	708	100.0	492	10 ADE93618	Ade93618 Human adi
2	708	100.0	537	10 ADE93667	Ade93667 Human adi
3	708	100.0	564	10 ADE93617	Ade93617 Human adi
4	708	100.0	582	10 ADE93616	Ade93616 Human adi
5	708	100.0	735	8 AAD56155	AAD56155 Human APM
6	708	100.0	735	10 ADC21966	ADC21966 Human ins

7	708	100.0	735	10 ADF16357	Adf16357 Human alb
8	708	100.0	735	10 ADF16359	Adf16359 Human alb
9	708	100.0	735	10 ADF16358	Adf16358 Human alb
10	708	100.0	735	10 ADE93611	Ade93611 Human adi
11	708	100.0	735	10 ADH21732	Adh21732 Human adi
12	708	100.0	735	10 ADH21734	Adh21734 Human HDA
13	708	100.0	735	10 ADH21733	Adh21733 Human HDA
14	708	100.0	735	12 ADF14853	Adf14853 Human art
15	708	100.0	742	10 ADD93529	Add93529 Novel nuc
16	708	100.0	754	10 ADD93525	Add93525 Novel nuc
17	708	100.0	778	10 ADD93527	Add93527 Novel nuc
18	708	100.0	783	10 ADD93521	Add93521 Novel nuc
19	708	100.0	1550	10 ADF94923	Adf94923 Human gen
20	708	100.0	4517	4 AAD10373	Aad10373 Human APM
21	708	100.0	4517	6 ABL67201	ABl67201 Thyroid c
22	708	100.0	4517	6 ABA96120	Aba96120 Human apm
23	708	100.0	4517	6 ABL10832	ABl10832 Human bre
24	708	100.0	4517	8 AAL60689	Aal60689 Human OBG
25	708	100.0	4517	12 ADF72537	Adf72537 Human OBG
26	708	100.0	4517	12 ADG14698	Adg14698 Human OBG
27	708	100.0	4517	12 ADQ18230	Adq18230 Human sof
28	708	100.0	4517	12 ADQ22777	Adq22777 Human sof
29	708	100.0	4545	3 AAD00553	Aad00553 Human APM
30	708	100.0	4545	6 AAI69247	Aai69247 Human APM
31	708	100.0	4545	10 ADD93523	Add93523 Novel nuc
32	708	100.0	20966	3 AAD00552	Aad00552 Human APM
33	708	100.0	20966	4 AAD10374	Aad10374 Human APM
34	708	100.0	20966	6 ABA96121	Aba96121 Human nuc
35	708	100.0	20966	6 AAI69243	Aai69243 Human APM
36	708	100.0	20966	8 AAL60690	Aal60690 Human OBG
37	708	100.0	20966	12 ADF72541	Adf72541 Human OBG
38	703	99.3	537	10 ADE93670	Ade93670 Human adi
39	703	99.3	537	10 ADE93665	Ade93665 Human adi
40	702	99.2	537	10 ADE93664	Ade93664 Human adi
41	702	99.2	537	10 ADE93666	Ade93666 Human adi
42	701	99.0	1313	2 AAT51049	Aat51049 Human adi
43	700	98.9	537	10 ADE93669	Ade93669 Human adi
44	699	98.7	411	10 ACC83228	Acc83228 N-termina
45	699	98.7	537	10 ADE93671	Ade93671 Human adi

ALIGNMENTS

RESULT 1
ADE93618
ID ADE93618 standard; CDNA; 492 BP.
XX
AC ADE93618;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human adiponectin apM1 (82-244) CDNA.

adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
antirheumatic; antibacterial; antilipaemic; dermatological;
KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
KW atherosclerosis; cardiovascular disease; dyslipidaemia;
KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
KW myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
wild-type.

OS Homo sapiens.
XX
PN WO2003055916-A2.
XX
PD 10-JUL-2003.

XX 20-DEC-2002; 2002WO-DK000897.
XX PF
XX 21-DEC-2001; 2001DK-00001952.
XX PR
XX 21-DEC-2001; 2001US-0343482P.
XX PR
XX 25-APR-2002; 2002DK-00000627.

PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogness A;
 XX
 DR WPI; 2003-598262/56.
 XX P-PSDB; ADE93612.
 XX
 XX New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX
 PS Claim 63; SEQ ID NO 16; 184pp; English.
 XX
 CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, immunomodulator and anorectic,
 CC dermatological, immunosuppressive, antibacterial, antilipaeamic,
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 cDNA of the
 CC invention.
 XX
 SQ Sequence 492 BP; 130 A; 128 C; 119 G; 115 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 7,898-86 Length: 492
 Scores: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1.0 Gaps: 0

US-10-072-159-11 (1-130) X ADE93618 (1-492)

QY 1 PheSerValGlyLeuGluThrTyValThrIleProAsnMetProIleArgPheThrLys 20
 Db 100 TTCAGTGTGGATTGGAGCTTACTTACTATCCCAACATGCCCATTCCTTTACCAAG 159
 QY 21 IlePheTyArgGlnGlnAsnHisTyArgGlySerThrGlyLysPheHisCysAsnIle 40
 Db 160 ATCTTCTACATCATGCAACCACTATGATGGCTCCACTGGTAATTCCTGCAACATT 219
 QY 41 ProGlyLeuTyTyPheAlaTyHisIleThrValTyMetLysAspValLysValSer 60
 Db 220 CCTGGGTGTACTACTTGGCTACCATCATCATGCTATATGAAGGATGGAAGGTCAGC 279
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyArgGlnTyArgGlnGluAsnVal 80
 Db 280 CTCTTCAAGAGGACCAAGGCTATGCTCTTCCCTATGATGATGACGAGGAATAATATGTG 339
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 340 GACCAGGCTCCGGCTCTGTGCTCTGCTCTGCTGAGGTGGCGACCAAGTCTGGCTCCAG 399
 QY 101 ValTyGlyGluGlyGluArgGlnGlyLeuTyAlaAspAsnAspAsnSerThrPhe 120

Db 400 GTGTATGGGAGGAGGAGCGCTAATGGACTCTATGTCTGTAATGACAATGACTCCACTTC 459
 QY 121 ThrGlyPheLeuLeuTyHisAspThrAsn 130
 Db 460 ACAGGCTTCTTCTCTACCATGACACCAAC 489
 RESULT 2
 ADE93667
 ID ADE93667 standard; cDNA; 537 BP.
 XX
 AC ADE93667;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 XX Human adiponectin Y11N-apM1 (82-244) mutant cDNA.
 DE
 XX
 KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antirheumatic; antibacterial; antilipaeamic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1; mutant;
 XX ss; gene.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003055916-A2.
 XX
 XX 10-JUL-2003.
 XX
 XX 20-DEC-2002; 2002WO-DK000897.
 PD
 XX
 PF 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0325492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 XX (MAXY-) MAXYGEN APS.
 XX (MAXY-) MAXYGEN HOLDINGS LTD.
 PA
 XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogness A;
 PI
 XX
 DR WPI; 2003-598262/56.
 DR P-PSDB; ADE93655.
 XX
 XX New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX
 PS Claim 63; SEQ ID NO 65; 184pp; English.
 XX
 CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, immunomodulator and anorectic,
 CC dermatological, immunosuppressive, antibacterial, antilipaeamic,
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC

CC current sequence is that of the human adiponectin apM1 (82-244) mutant
 CC cDNA of the invention.

XX
 SQ Sequence 537 BP; 135 A; 139 C; 132 G; 131 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8, 9e-86 Length: 537
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADE93667 (1-537)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 145 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 204
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 205 ATCTTCTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAATTCCTGCAACATT 264
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 265 CTGGGCTGTACTCTTGGCTTACCAATCAGCTATATGAAGGATGTGAAGGTCCAGC 324
 QY 61 LeuPheLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 325 CTCTTCAGAGGACGACGATGCTCTCCATATGATGATGATGATGATGATGATGATG 384
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisIleGluValGlyAspGlnValTyrLeuGln 100
 Db 385 GACCAAGGCTCCGGCTCTGTGCTCTGATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 444
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
 Db 445 GTGTATGGGAGGAGGAGCGTAATGACTCTATGCTGATATGATGATGATGATGATG 504
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 505 ACAGGCTTCTCTCTTACCATGACACCAAC 534

RESULT 3

ADE93617

ID ADE93617 standard; cDNA; 564 BP.

AC ADE93617;

XX 12-FEB-2004 (first entry)

DE Human adiponectin apM1 (58-244) cDNA.

KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiatic;
 KW antirheumatic; antibacterial; antilipemic; anorectic; diabetes; obesity;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
 KW wild-type.

OS Homo sapiens.

XX WO2003055916-A2.

XX 10-JUL-2003.

XX 20-DEC-2002; 2002WO-BK000897.

XX 21-DEC-2001; 2001DX-00001952.

XX 21-DEC-2001; 2001US-0343482P.

XX 25-APR-2002; 2002DK-0000062P.

PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogness A;
 XX WPI: 2003-598262/56.
 DR P-PSDB; ADE93615.

XX New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX Claim 63; SEQ ID NO 15; 184pp; English.

XX The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC antidiabetic, cardiant, antirheumatic, antibacterial, antilipemic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apM1 cDNA of the
 CC invention.

SQ Sequence 564 BP; 150 A; 140 C; 145 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9, 53e-86 Length: 564
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADE93617 (1-564)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 172 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 231
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 232 ATCTTCTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAATTCCTGCAACATT 291
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 292 CTGGGCTGTACTCTTGGCTTACCAATCAGCTATATGATGATGATGATGATGATGATG 351
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 352 CTCTTCAGAGGACGACGATGCTCTCCATATGATGATGATGATGATGATGATGATG 411
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisIleGluValGlyAspGlnValTyrLeuGln 100
 Db 412 GACCAAGGCTCCGGCTCTGTGCTCTGATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 471
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120

[illegible]

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 583 GACCAGCCCTCCGGCTCTGTGCTCCATCTGGAGTGGCGCACCAAGTCTGGCTCCAG 642
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
 Db 643 GTGTATGGGAGAGAGAGGCTATGACCTATGCTGATAATGACAATGACTCCACCTTC 702
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 703 ACAGGCTTCTTCTCTACCATGACACCAAC 732

RESULT 7

ADFI6357
 ID ADFI6357 standard; DNA; 735 BP.

XX AC ADFI6357;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human albumin fusion protein-related DNA sequence SeqID1449.
 XX KW albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.
 XX OS Homo sapiens.
 XX PN WO2003060071-A2.
 XX PD 24-JUL-2003.
 XX PF 23-DEC-2002; 2002WO-US040891.

XX 21-DEC-2001; 2001US-0341811P.
 PR 24-JAN-2002; 2002US-0350358P.
 PR 28-JAN-2002; 2002US-0351360P.
 PR 26-FEB-2002; 2002US-0359370P.
 PR 28-FEB-2002; 2002US-0360000P.
 PR 27-MAR-2002; 2002US-0367500P.
 PR 08-APR-2002; 2002US-0370227P.
 PR 10-MAY-2002; 2002US-0378950P.
 PR 24-MAY-2002; 2002US-0382617P.
 PR 28-MAY-2002; 2002US-0383123P.
 PR 05-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.

(HUMA-) HUMAN GENOME SCI INC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.

XX FI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
 XX WPI; 2003-598517/56.
 XX P-PSDB; ADFI6683.

XX New albumin fusion protein, useful for preparing a composition for
 XX treating diabetes mellitus.

XX Example 4; SEQ ID NO 1449; 24pp; English.

XX This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also

CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
 CC therapeutic protein which was fused with human albumin to create a novel
 CC albumin fusion protein of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/publishedpcpt_sequences

SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-38e-85 Length: 735
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADFI6357 (1-735)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 343 TTCAGTGTGGATTGGAGACTTACGTTACTATCCCCAACATGCCATTCCGTTTACCAAG 402
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyValPheHisCysAsnIle 40
 Db 403 ATCTTCTCAATCAGCAAAACCACTAATGAGTCCCTCCTGGTAAATTCCTCCTGCAACATT 462
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 463 CCTGGGCTGTACTTTCCTTACCACATCACAGTCTATATCAAGAGTGTGAAGTCAGC 522
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 523 CTCTTCAAGAGACAAAGCTATGCTTTCACCTATGATCAGTACCAAGAAATAATGTG 582
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 583 GACCAGGCTCCGGCTCTGTGCTCTCGCATCTGGAGTGGCGCACCAAGTCTGGCTCCAG 642
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
 Db 643 GTGTATGGGAGAGAGAGCGTAAATGAGCTCTATGCTGATAATGACAATGACTCCACCTTC 702
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 703 ACAGGCTTCTTCTCTACCATGACACCAAC 732

RESULT 8

ADFI6359
 ID ADFI6359 standard; DNA; 735 BP.

XX AC ADFI6359;
 XX DT 12-FEB-2004 (first entry)

XX DE Human albumin fusion protein-related DNA sequence SeqID1451.
 XX KW albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.
 XX OS Homo sapiens.

XX PN WO2003060071-A2.

XX PD 24-JUL-2003.

PF 23-DEC-2002; 2002WO-US040891.
 XX 21-DEC-2001; 2001US-0341811P.
 PR 24-JAN-2002; 2002US-0350358P.
 PR 26-JAN-2002; 2002US-0351360P.
 PR 28-FEB-2002; 2002US-0359370P.
 PR 28-FEB-2002; 2002US-0360000P.
 PR 27-MAR-2002; 2002US-0367500P.
 PR 08-APR-2002; 2002US-0370227P.
 PR 10-MAY-2002; 2002US-0378950P.
 PR 24-MAY-2002; 2002US-0382617P.
 PR 28-MAY-2002; 2002US-0383123P.
 PR 05-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 FA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA,
 PI WPI; 2003-598517/56.
 XX P-PSDB; ADF16685.
 DR New albumin fusion protein, useful for preparing a composition for
 XX treating diabetes mellitus.
 PS Example 4; SEQ ID NO 1451; 24pp; English.
 CC This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition which encodes a
 CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
 CC therapeutic protein which was fused with human albumin to create a novel
 CC albumin fusion protein of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publishedpct_sequences
 XX SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;
 Alignment Scores:
 P-red. No.: 1.38e-85 Length: 735
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-072-159-11 (1-130) x ADF16359 (1-735)
 QY 1 PheSerValGlyLeuGluThrValThrIleProAsnMetProIleArgPheThrLys 20
 DB 343 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 402
 QY 21 IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 403 ATCTTCTCAATCAGCAAAACCACATGATGCTCCATGGTAATTCACCTGCAACATT 462

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 DB 463 CTGGGCTGTACTCTTTGGCTCTACCATCAGCTCTATATGAAGSATGTGAGGTCAGC 522
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 DB 523 CTCCTTCAAGAAGGAGCAAGCTATGCTTTCACCTATGATCAGTACCAGGAAAAATAATGTG 582
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 DB 583 GACCAAGGCTCCGGCTCTGTCTCTGCACTCTGGAGGTGGGGACCAAGTCTGGCTCCAG 642
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
 DB 643 GTGTATGGGAGGAGAGCGTAATGGACTCTATGCTGATATGATGATGATGATGATGATG 702
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 DB 703 ACAGGCTTCTCTCTCTACCATGACCAAC 732
 RESULT 9
 ADF16358
 ID ADF16358 standard; DNA; 735 BP.
 XX ADF16358;
 AC ADF16358;
 XX 12-FEB-2004 (first entry)
 DT Human albumin fusion protein-related DNA sequence SeqID1450.
 XX albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.
 XX Homo sapiens.
 OS
 XX WC2003060071-A2.
 XX 24-JUL-2003.
 XX 23-DEC-2002; 2002WO-US040891.
 XX 21-DEC-2001; 2001US-0341811P.
 PR 24-JAN-2002; 2002US-0350358P.
 PR 28-JAN-2002; 2002US-0351360P.
 PR 28-FEB-2002; 2002US-0359370P.
 PR 28-FEB-2002; 2002US-0360000P.
 PR 27-MAR-2002; 2002US-0367500P.
 PR 08-APR-2002; 2002US-0370227P.
 PR 10-MAY-2002; 2002US-0378950P.
 PR 24-MAY-2002; 2002US-0382617P.
 PR 28-MAY-2002; 2002US-0383123P.
 PR 05-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 FA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA,
 PI WPI; 2003-598517/56.
 DR P-PSDB; ADF16684.

XX New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 PS Example 4; SEQ ID NO 1450; 24pp; English.
 XX
 CC This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
 CC therapeutic protein which was fused with human albumin to create a novel
 CC albumin fusion protein of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publishedpt_sequences
 XX
 SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.38e-85 Length: 735
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADF16358 (1-735)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 402
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 403 ATCTTCAACATCAGCAACCAACACATATGATGCTCCATGTTAAATTCATTCGCAACATT 462
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 463 CCTGGCGCTGATCTACTTTCCTTACCACATCATCAGTCTATATCAAGGATGTGAAGTCAGC 522
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnLysAsnVal 80
 Db 523 CTCTTCAAGAGGACAGGCTATGCTCTTACCTATGATCAGTACCGAGAAATAATGTG 582
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 583 GACCAGGCTCTCGGCTCTGTCTCTGCTATCGATCTGGAGTGGCGACCAAGTCTGGCTCCAG 642
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
 Db 643 GTGTATGGGAGGAGAGCGTAATGGACTCTATGCTGATATGATCAATGACTCCACCTTC 702
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 703 ACAGGCTTCTCTCTACCATGACACCAAC 732

RESULT 10
 ADE93611
 ID ADE93611 standard; cDNA; 735 BP.
 XX
 AC ADE93611;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human adiponectin apM1 (1-244) cDNA.
 XX
 KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;

KW antirheumatic; antibacterial; antilipaeamic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apM1; ss; gene;
 KW wild-type.
 XX
 OS Homo sapiens.
 XX
 PN WO2003055916-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 20-DEC-2002; 2002WO-DK000897.
 XX
 PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 03-JUL-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 20-SEP-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bogsgnes A;
 XX
 DR WPI; 2003-598262/56.
 DR P-PSDB; ADE93603.
 XX

New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 Disclosure; SEQ ID NO 9; 184pp; English.
 The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the adiponectin polypeptide. The adiponectin polypeptide comprises an amino acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent adiponectin is occupied by a surface exposed amino acid residue. The conjugate of the invention demonstrates antiarteriosclerotic, antidiabetic, cardiant, antirheumatic, antibacterial, antilipaeamic, dermatological, immunosuppressive, immunomodulator and anorectic activities and may be useful for treating diabetes, obesity, atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren syndrome, cachexia, septic shock, myasthenia gravis, myocardial infarction and destructive processes related to activation of the inflammatory system, as well as during gene therapy procedures. The current sequence is that of the human adiponectin apM1 cDNA of the invention.
 SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.38e-85 Length: 735
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADE93611 (1-735)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 343 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 402

XX	PT	New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.		
XX	PS	Disclosure; SEQ ID NO 529; 1086pp; English.		
XX	CC	The invention relates to fusion proteins comprising human serum albumin (ADH21530) and a therapeutic polypeptide such as a therapeutic protein, antibody or peptide or their variants or fragments. The therapeutic protein may be fused to the N-terminus, the C-terminus or both termini of albumin via a linker. The albumin component of the fusion proteins prolongs the shelf-life and the in vitro and vivo biological activity of the proteins compared with those of the corresponding therapeutic proteins on their own. The invention also relates to nucleic acids encoding albumin fusion proteins, vectors and host cells comprising an albumin fusion protein, nucleic acid, compositions and kits comprising an albumin fusion protein, the method of extending the shelf-life of a therapeutic protein by fusion with albumin, and the treatment of disease using an albumin fusion protein. The albumin fusion proteins may be used in the treatment of metabolic/endocrine disorders, diabetes and diabetes-related conditions. Specifically the albumin fusion proteins may be used to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders (especially neuropathy), retinopathy, cardiovascular disorders (especially heart disease), renal disorders and obesity. The proteins may also be used in a method of maintaining a basal glucose level in a patient and in a method for losing weight. The present sequence is related to the invention.		
XX	SEQ	Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;		
		Alignment Scores:		
	Pred. No.:	1.38e-85	Length:	735
	Score:	708.00	Matches:	130
	Percent Similarity:	100.00%	Conservative:	0
	Best Local Similarity:	100.00%	Mismatches:	0
	Query Match:	100.00%	Indels:	0
	DB:	10	Gaps:	0
		US-10-072-159-11 (1-130) x ADH21732 (1-735)		
QY	1	PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys	20	
Db	343	TTCAAGTGGGATGGAGACTTACGTTACTATCCCAACATGCCATTCGCTTTACCAAG	402	
QY	21	IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle	40	
Db	403	ATCTTCTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAATTCCTACTGCAACATT	462	
QY	41	ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer	60	
Db	463	CCTGGGCTGTACTTACITTTGCTTACCACATCACAGTCTATATGAAGGATGTGAAGGTCCAG	522	
QY	61	LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal	80	
Db	523	CTCTTCAAGAGCAAGGCTATGCTCTTCCACTATGATCAGTACCAAGAAATAATGTG	582	
QY	81	AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln	100	
Db	583	GACCAGGCTCCGGCTCTGTGCTCTCCATCTGGAGGTGGGACCAAGTCTGGCTCCAG	642	
QY	101	ValTyrGlyGluGlyAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnValTrpLeuGln	120	
Db	643	GTGTATGGGAAGGAGAGCGTATGACTCTATGCTGATAATGACATGACTCCACTTC	702	
QY	121	ThrGlyPheLeuLeuTyrHisAspThrAsn	130	
Db	703	ACAGGCTTTCTCTTACCATGACACCAAC	732	
		RESULT 12		
		ADH21734		
	ID	ADH21734 standard; DNA; 735 BP.		
XX	AC	ADH21734;		

XX DT 11-MAR-2004 (first entry)

XX DE Human HDALV07-encoding DNA, SEQ ID NO:531.

XX KW Fusion protein; human serum albumin; HSA; therapeutic protein; shelf-life; in vitro biological activity; in vivo biological activity; metabolic disorder; endocrine disorder; diabetes; type 1; type 2; diabetes-related condition; hyperglycaemia; neural disorder; neuropathy; retinopathy; cardiovascular disorder; heart disease; renal disorder; obesity; glucose level maintenance; weight loss; antidiabetic; cardiant; anorectic; ophthalmological; gene therapy; gene; ds.

XX OS Homo sapiens.

XX PN WO2003059934-A2.

XX PD 24-JUL-2003.

XX PF 23-DEC-2002; 2002WO-US040892.

XX PR 21-DEC-2001; 2001US-034181P.

PR 24-JAN-2002; 2002US-0350358P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX FA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Haseltine WA;

XX DR WPI: 2003-598501/56.

DR P-PSDB; ADH21886.

XX PT New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.

XX PS Disclosure; SEQ ID NO 531; 1086pp; English.

XX CC The invention relates to fusion proteins comprising human serum albumin (ADH21530) and a therapeutic polypeptide such as a therapeutic protein, antibody or peptide or their variants or fragments. The therapeutic protein may be fused to the N-terminus, the C-terminus or both termini of albumin via a linker. The albumin component of the fusion proteins prolongs the shelf-life and the in vitro and vivo biological activity of the proteins compared with those of the corresponding therapeutic proteins on their own. The invention also relates to nucleic acids encoding albumin fusion proteins, vectors and host cells comprising an albumin fusion protein nucleic acid, compositions and kits comprising an albumin fusion protein, the method of extending the shelf-life of a therapeutic protein by fusion with albumin, and the treatment of disease using an albumin fusion protein. The albumin fusion proteins may be used in the treatment of metabolic/endocrine disorders, diabetes and diabetes-related conditions. Specifically the albumin fusion proteins may be used to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders (especially neuropathy), retinopathy, cardiovascular disorders (especially heart disease, renal disorders and obesity). The proteins may also be used in a method of maintaining a basal glucose level in a patient and in a method for losing weight. The present sequence is related to the invention.

XX SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.38e-85 Length: 735

Score: 708.00 Matches: 130

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADH21734 (1-735)

QY 1 PheSerValGlyLeuGluThrValThrIleProAsnMetProIleArgPheThrLys 20

Db 343 TTCAGTGTGGGATTGGAGACTTACGTTACTATATCCCAACATGCCCATTCGCTTTACCAAG 402

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40

Db 403 ATCTTCTACCAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTACTCCACATT 462

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60

Db 463 CCTGGGCTGTACTATTGCTTACCACATCAGTCTATATGAAGGATGTGAAGGTCAGC 522

QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80

Db 523 CTCTTCAGGAAGGACCAAGGCTATGCTCTTACCTATGATCAGTACCAAGGAAATATATGTG 582

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100

Db 583 GACCAGGCTCCGGCTCTGTGCTCTGCTCATCTGGAGTGGGGAGCAAGTCTGGCTCCAG 642

QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120

Db 643 GTGTATGGGGAAGGAGAGCGTAAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 702

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130

Db 703 ACAGGCTTTCTCTCTACCATGACACCAAC 732

RESULT 13

ADH21733

ID ADH21733 standard; DNA; 735 BP.

XX AC

XX ADH21733;

XX DT 11-MAR-2004 (first entry)

XX DE Human HDALV07 (GD)/adiponectin-encoding DNA, SEQ ID NO:530.

XX KW Fusion protein; human serum albumin; HSA; therapeutic protein; shelf-life; in vitro biological activity; in vivo biological activity; metabolic disorder; endocrine disorder; diabetes; type 1; type 2; diabetes-related condition; hyperglycaemia; neural disorder; neuropathy; retinopathy; cardiovascular disorder; heart disease; renal disorder; obesity; glucose level maintenance; weight loss; antidiabetic; cardiant; anorectic; ophthalmological; gene therapy; gene; ds.

XX OS Homo sapiens.

XX PN WO2003059934-A2.

XX PD 24-JUL-2003.

XX PF 23-DEC-2002; 2002WO-US040892.

XX PR 21-DEC-2001; 2001US-034181P.

PR 24-JAN-2002; 2002US-0350358P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 02-OCT-2002; 2002US-041984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX
PA (HUVA-) HUMAN GENOME SCI INC.
XX Rosen CA, Haseltine WA;
XX WPI; 2003-598501/56.
XX P-PSDB; ADH21885.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Disclosure; SEQ ID NO 530; 1086pp; English.

The invention relates to fusion proteins comprising human serum albumin (ADH21530) and a therapeutic polypeptide such as a therapeutic protein, antibody or peptide or their variants or fragments. The therapeutic protein may be fused to the N-terminus, the C-terminus or both termini of albumin via a linker. The albumin component of the fusion proteins prolongs the shelf-life and the in vitro and vivo biological activity of the proteins compared with those of the corresponding therapeutic proteins on their own. The invention also relates to nucleic acids encoding albumin fusion proteins, vectors and host cells comprising an albumin fusion protein nucleic acid, compositions and kits comprising an albumin fusion protein, the method of extending the shelf-life of a therapeutic protein by fusion with albumin, and the treatment of disease using an albumin fusion protein. The albumin fusion proteins may be used in the treatment of metabolic/endocrine disorders, diabetes and diabetes related conditions. Specifically the albumin fusion proteins may be used to treat type 1 and type 2 diabetes, hyperglycaemia, neural disorders (especially neuropathy), retinopathy, cardiovascular disorders (especially heart disease), renal disorders and obesity. The proteins may also be used in a method of maintaining a basal glucose level in a patient and in a method for losing weight. The present sequence is related to the invention.

XX
SQ Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,386-85 Length: 735
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADH21733 (1-735)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProfileArgPheThrLys 20
Db 343 TTCAGTTGGGATTGGAGACTTAGCTTACTATCCCAACATGCCCATTCGCCTTTACCAG 402
QY 21 IlePheTyraSngInGlnAAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 403 AICTTCTACATCACAPAAACCACTATGAATGGCTCCACTGGTAATTCCTCGACTGCACATT 462
QY 41 ProGlyLeuTyrTy-PheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 463 CTGTGGGCTGTACTCTTTTGCCCTACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGC 522
QY 61 LeuPheLysLyAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 523 CTCITTCAGAAGGACAAGGCTATGCTCTTCACCTATGATCATACAGGAATAATATGTG 582
QY 81 AspGlnAlaserGlyserValLeuLeuHisIleSngGluValGlyAspGlnValTrpLeuGln 100
Db 583 GACACGGCTCCGGCTCTGTGCTCTGATCTGGAGGTGGGCGCACCAAGTGTGGCTCCAG 642

QY	101	ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe	121
Db	643	GGTATGGGGAAGAGAGCGTAATGGACTCTATGCTGATATGACANTGACTCCACCTTC	702
QY	121	ThrGlyPheLeuLeuTyrHisAspThrAsn 130	
Db	703	ACAGGCTTCTCTCTACCATGACCAAC 732	
RESULT 14			
ADFL14853	ADFL14853 standard; DNA; 735 BP.		
XX	ADFL14853		
XX	ADFL14853;		
XX			
DT	26-FEB-2004 (first entry)		
XX			
DE	Human arteriosclerosis-related protein coding sequence, SEQ ID 1.		
XX			
KW	Arteriosclerosis; adiponectin; scavenger receptor A ;		
KW	antiarteriosclerotic; human; gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..735	
FT		/*tag= a	
FT		/product= "Human arteriosclerosis-related protein"	
XX			
PN	WO2003099319-A1.		
XX			
PD	04-DEC-2003.		
XX			
FF	26-MAY-2003; 2003WO-JP006518.		
XX			
PR	24-MAY-2002; 2002JP-00151220.		
XX			
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.		
XX			
PI	Kadowaki T, Yamauchi T, Kubota N, Terauchi Y, Kubota T, Noda T;		
PI	Nagai R, Inai Y;		
XX			
DR	WPI; 2004-023231/02.		
XX	P-PSDB; ADFL14854.		
PT	Preventives or remedies for arteriosclerosis containing agents for		
PT	regulating scavenger receptor A expression in arterial walls to inhibit		
PT	lipid accumulation in macrophages and to prevent its onset and		
PT	progression.		
XX			
PS	Disclosure; SEQ ID NO 1; 46pp; Japanese.		
XX			
CC	The present invention relates to preventives or remedies for		
CC	arteriosclerosis, which contain as active ingredient a spherical region		
CC	in the C-terminal side of adiponectin, adiponectin or their gene. Such		
CC	drugs contain agents for regulating scavenger receptor A expression in		
CC	arterial wall to inhibit lipid accumulation in macrophages and to prevent		
CC	onset and progression of arteriosclerosis with direct stoppage of		
CC	endothelium form thickening. The present sequence was used to illustrate		
CC	the invention.		
XX			
SQ	Sequence 735 BP; 179 A; 193 C; 201 G; 162 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	1,38e-85	Length:	735
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-072-159-11 (1-130) x ADF14853 (1-735)

1 p h e s e r v a l g l y l e u g l u t h r t y r v a l t h r i l e p r o a s n m e t p r o i l e a r g p h e t h r l y s 20

1 p h e s e r v a l g l y l e u g l u t h r t y r v a l t h r i l e p r o a s n m e t p r o i l e a r g p h e t h r l y s 20

Db 343 TTCAGTGTGGATTGGAGACTTACGTTACTATCCCAACATGCCATTCGCTTTACCAAG 402
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 403 ATCTTCTCAATCAGCAAAACCACTATGATGCTCCACTGGTAAATTCCTGCAACATT 462
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 463 CTGGGCTGTACTACTTTGCTTCCACATCAGATCTATGAGAGATGTGAGGTCCAGC 522
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 523 CTCCTTCAAGAGACAAAGCTATGCTTTCACCTATGATCAGTACCAAGGAAATAATGTG 582
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
 Db 583 GACCAGGCTCCGGCTCTGTCTCTGATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 642
 QY 101 ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
 Db 643 GTGTATGGGAAGAGAGAGCGTAATGAGCTCTATGCTGATATGACATGACTCCACCTTC 702
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 703 ACAGGCTTCTCTCTTACCATGACACCAAC 732

RESULT 15

ADD93529
 ID ADD93529 standard; cdNA; 742 BP.

AC ADD93529;

DT 29-JAN-2004 (first entry)

XX DE Novel nucleic acid NOV2e, homologous to human adiponectin.

XX KW NOV2e; human; adiponectin; gene therapy; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 11..712

XX FT /*tag= a

XX FT /partial

XX FT /product= "Human NOV2e"

XX FT /note= "No start codon"

XX PN WO2003078572-A2.

XX PD 25-SEP-2003.

XX PF 06-MAR-2003; 2003WO-US006859.

XX PR 15-MAR-2002; 2002US-0365034P.

XX PR 19-MAR-2002; 2002US-0365477P.

XX PR 21-MAR-2002; 2002US-0366420P.

XX PR 05-MAR-2003; 2003US-00379747.

XX PA (CURA-) CURAGEN CORP.

XX PI Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Gangolli EA;

XX PI Malyankar UM, Miller CE, Ooi CE, Ort T, Patturajan M, Rastelli L;

XX PI Rieger DK, Shinkets RA, Zerhusen BD;

XX DR WPI; 2003-779122/73.

XX DR P-PSDB; ADD93530.

XX XX New isolated NOVX polypeptides and polynucleotides, useful for

XX PT preventing, diagnosing or treating NOVX-associated disorders, e.g.

XX PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

XX PT asthma, or infections.

XX XX

Claim 20; Page 108; 205pp; English.

XX The present sequence is that of a novel polynucleotide encoding novel
 CC NOV2e, a polypeptide that shows amino acid sequence homology to the human
 CC adiponectin (adipose most abundant gene transcript 1, APN1). The
 CC adiponectin gene is the most abundant gene transcript in adipose cells
 CC that regulates lipid metabolism. An interaction between adiponectin and
 CC calcium modulating ligand was identified, indicating a novel pathway by
 CC which adiponectin may induce lipid breakdown in muscle cells and
 CC adipocytes. The invention is based on the identification of proteins and
 CC polypeptides, and the nucleic acids encoding them, that are
 CC differentially modulated in a pathological state, disease or an abnormal
 CC condition or state. These are targets for therapeutic agents and can be
 CC used in screening methodologies to identify candidate therapeutic agents
 CC which interact with the target and thereby exert a desired or favourable
 CC effect, e.g. in neurogenesis, cell differentiation, cell proliferation,
 CC haematopoiesis, wound healing and angiogenesis. Methods for diagnosis,
 CC treatment and prevention of disorders involving the novel human nucleic
 CC acids and proteins are provided. The nucleic acids are further used in
 CC gene therapy, as hybridization probes and primers, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics.

SQ Sequence 742 BP; 189 A; 204 C; 197 G; 152 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.4e-85 Length: 742
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-072-159-11 (1-130) x ADD93529 (1-742)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 320 TTCAGTGTGGATTGGAGACTTACGTTACTATCCCAACATGCCATTCGCTTTACCAAG 379
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 380 ATCTTCTCAATCAGCAAAACCACTATGATGCTCCACTGGTAAATTCCTGCAACATT 439
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 440 CTGGGCTGTACTACTTTGCTTCCACATCAGTCTATATGAGGATGTGAGGTCCAGC 499
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 500 CTCCTTCAAGAGGACAAAGGCTATGCTTTCACCTATGATCAGTACCAAGAAATAATGTG 559
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
 Db 560 GACCAGGCTCCGGCTCTGTCTCTGATCTGGAGGTGGGCGACCAAGTCTGGCTCCAG 619
 QY 101 ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
 Db 620 GTGTATGGGAAGAGAGAGCGTAATGAGCTCTATGCTGATATGACATGACTCCACCTTC 679
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 680 ACAGGCTTCTCTCTTACCATGACACCAAC 709

Search completed: December 3, 2004, 11:01:11

Job time : 405 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2004, 09:58:48 ; Search time 2353 Seconds

(without alignments)
2612.691 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708

Sequence: 1 FSVGLETYTYINPMPIRFTK.....YADNDNDSTFTGFLLYHDIN 130

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -NATFIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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Database :

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4:	gb_om.*
5:	gb_ov.*
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8:	gb_pl.*
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13:	gb_un.*
14:	gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	708	100.0	492	6	AX800356 Sequence
2	708	100.0	521	9	HLA131461
3	708	100.0	537	6	AX800405 Sequence
4	708	100.0	564	6	AX800355

5	708	100.0	582	6	AX800354
6	708	100.0	735	6	AX752056
7	708	100.0	735	6	AX800349
8	708	100.0	1313	6	AF034253
9	708	100.0	4510	6	CQ715267
10	708	100.0	4517	6	AR138194
11	708	100.0	4517	6	AR255755
12	708	100.0	4517	6	AR337311
13	708	100.0	4517	6	AR343651
14	708	100.0	4517	6	AX195211
15	708	100.0	4517	6	AX335029
16	708	100.0	4517	6	AX358521
17	708	100.0	4517	6	AX767959
18	708	100.0	4517	6	AX951629
19	708	100.0	4517	6	AX960544
20	708	100.0	4517	6	BD074783
21	708	100.0	4517	9	HUMUFS12
22	708	100.0	4537	9	AB012163S3
23	708	100.0	4545	6	BD238086
24	708	100.0	4545	6	AR344520
25	708	100.0	4545	6	AX134174
26	708	100.0	13001	9	AC072018
27	708	100.0	20966	6	BD238082
28	708	100.0	20966	6	AR337312
29	708	100.0	20966	6	AR343652
30	708	100.0	20966	6	AR344516
31	708	100.0	20966	6	AX134170
32	708	100.0	20966	6	AX195213
33	708	100.0	20966	6	AX358523
34	708	100.0	20966	6	AX767961
35	708	100.0	20966	6	AX960548
36	708	100.0	176155	2	AC012149
37	708	100.0	195323	2	AC026612
38	707	99.9	734	9	AF404407
39	703	99.3	537	6	AX800403
40	703	99.3	537	6	AX800408
41	702	99.2	537	6	AX800402
42	702	99.2	537	6	AX800404
43	700	98.9	537	6	AX800407
44	699	98.7	537	6	AX800406
45	699	98.7	537	6	AX800409

ALIGNMENTS

RESULT 1	AX800356	492 bp	DNA	linear	PAT 13-OCT-2003
AX800356	Sequence 16 from Patent WO03055916.				
LOCUS	AX800356				
DEFINITION	Sequence 16 from Patent WO03055916.				
ACCESSION	AX800356				
VERSION	AX800356.1	GI:37653576			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T., Halkier,T. and Boggsnes,A.				
TITLE	Adiponectin fragments and conjugates				
JOURNAL	Patent: WO 03055916-A 16 10-JUL-2003;				
	Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers (Cayman) Limited (KY)				
FEATURES	Location/Qualifiers				
source	1..492				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
	/note="apM1 (82-244) coding sequence"				

ORIGIN

Alignment Scores:

Prd. No.: 2.42e-74

Length: 492

Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-072-159-11 (1-130) x AX800356 (1-492)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrIys 20
 DB 100 TTCAAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGTTTACCAAG 159
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 160 ATCTTCTACATCAGCAAAACCACTATGATGCTCCATGGTAAATCCACTGCAACATT 219
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 DB 220 CTTGGGCTGACTACTTCTGGCTTACCACATCAGCTCTATATGAAGATGTGAAGTTCAGC 279
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 DB 280 CTCCTTCAAGAGGACCAAGCTATGCTCTTCCCTATGATCATGATCCAGGAAAAATAATGTG 339
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
 DB 340 GACCAAGGCTCGGCTCTGTGCTCTGCTATCTGGAGGTGGGACCAAGTCTGGCTCCAG 399
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
 DB 400 GTGTATGGGAGGAGGAGCGTAATGGACTCTATGCTGATGATGATGATGATGATGATGATG 459
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 DB 460 ACAGGCTTCTCTCTACATGACACCAAC 489

RESULT 2
 HSA131461
 LOCUS Homo sapiens apM-1 gene, exon 3. 521 bp DNA linear PRI 21-OCT-1999
 DEFINITION AJ131461
 ACCESSION AJ131461
 VERSION AJ131461.1 GI:5725240
 KEYWORDS adipocyte-specific secretory protein; apM-1 gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Schaffler, A., Orso, E., Palitzsch, K.D., Buchler, C., Drobnik, W., Furst, A., Scholmerich, J. and Schmitz, G.
 TITLE The human apM-1, an adipocyte-specific gene linked to the family of TNF's and to genes expressed in activated T cells, is mapped to chromosome 1q21.3-q23, a susceptibility locus identified for familial combined hyperlipidaemia (FCH)
 JOURNAL Biochem. Biophys. Res. Commun. 260 (2), 416-425 (1999)
 MEDLINE 99333693
 PubMed 10403784
 REFERENCE 2 (bases 1 to 521)
 AUTHORS Schaffler, A.J.
 TITLE Direct Submission
 JOURNAL Submitted (09-DEC-1998) Schaffler A.J., University of Regensburg, Germany, Institute for Clinical Chemistry and Laboratory Medicine, Franz-Josef-Strauss-Allee 11, D-93042, GERMANY

FEATURES
 source
 1..521
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="1"
 /map="1q21.3-q23"
 1..521
 /gene="apM-1"
 1..>521

gene
 exon

/gene="apM-1"
 /number=3
 /usedin=AJ131460:apM1_CDS

ORIGIN

Alignment Scores:
 Pred. No.: 2,58e-74 Length: 521
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-072-159-11 (1-130) x HSA131461 (1-521)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrIys 20
 DB 129 TTCAGTGTGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGTTTACCAAG 188
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 189 ATCTTCTACATCAGCAAAACCACTATGATGCTCCATGGTAAATCCACTGCAACATT 248
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 DB 249 CTTGGGCTGACTACTTCTGGCTTACCACATCAGCTCTATATGAAGATGTGAAGTTCAGC 308
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 DB 309 CTCCTTCAAGAGGACCAAGCTATGCTCTTCCCTATGATCATGATCCAGGAAAAATAATGTG 368
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
 DB 369 GACCAAGGCTCGGCTCTGTGCTCTGCTATCTGGAGGTGGGACCAAGTCTGGCTCCAG 428
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
 DB 429 GTGTATGGGAGGAGGAGCGTAATGGACTCTATGCTGATGATGATGATGATGATGATGATG 488
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 DB 489 ACAGGCTTCTCTCTACATGACACCAAC 518

RESULT 3

AX800405
 LOCUS AX800405 537 bp DNA linear PAT 13-OCT-2003
 DEFINITION Sequence 65 from Patent WO03055916.
 ACCESSION AX800405
 VERSION AX800405.1 GI:37653580
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Rasmussen, P.B., Andersen, K.V., Pedersen, A.H., Schambye, H.T., Halkier, T. and Bogesnes, A.
 TITLE Adiponectin fragments and conjugates
 JOURNAL Patent: WO 03055916-A 65 10-JUL-2003;
 Maxygen Aps (DK); Maxygen Holdings Ltd. c/o Close Brothers (Cayman) Limited (KY)
 FEATURES
 Location/Qualifiers
 1..537
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic construct encoding Villin-apM1 (82-244)"

ORIGIN

Alignment Scores:
 Pred. No.: 2,68e-74 Length: 537
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-072-159-11 (1-130) x AX800405 (1-537)

QY 1 PheSerValGlyLeuGluThyValThrIleProAsnMetProIleArgPheThrLys 20
DB 145 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 204
QY 21 IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
DB 205 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGTTAAATTCCTGCAACATT 264
QY 41 ProGlyLeuTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60
DB 265 CTTGGCTGTACTACTTTGGCTACCACTACATCATGATATGAAGGATGTGAAGGTCAGC 324
QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
DB 325 CTCTTCAAGAGGACCAAGGCTATGCTCTTCACTATGATCAGTACCAAGAAATATATGTG 384
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
DB 385 GACCAAGGCTCGGCTCTGCTCTCTGCACTGGAGGTGGCGGACCAAGTCTGGCTCCAG 444
QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
DB 445 GTGTATGGGAGGAGAGCGTAATGGACTCTATGCTGATGATGATGATGATGATGATGATG 504
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
DB 505 ACAGGCTTCTCTCTACCATGACCAAC 534

RESULT 4
LOCUS AX800355 564 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 15 from Patent WO03055916.
ACCESSION AX800355
VERSION AX800355.1 GI:37653575
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
AUTHORS Haikier,T. and Bogness,A.
TITLE Adiponectin fragments and conjugates
JOURNAL Patent: WO 03055916-A 15 10-JUL-2003;
Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
(Cayman) Limited (KY)
FEATURES
source
Location/Qualifiers
1..564
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="apM1(58-244) coding sequence"

ORIGIN
Alignment Scores:
Pred. No.: 2,848-74 Length: 564
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-072-159-11 (1-130) x AX800355 (1-564)

QY 1 PheSerValGlyLeuGluThyValThrIleProAsnMetProIleArgPheThrLys 20
DB 172 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 231

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-072-159-11 (1-130) x AX800405 (1-537)

QY 21 IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
DB 205 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGTTAAATTCCTGCAACATT 264
QY 41 ProGlyLeuTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60
DB 265 CTTGGCTGTACTACTTTGGCTACCACTACATCATGATATGAAGGATGTGAAGGTCAGC 324
QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
DB 325 CTCTTCAAGAGGACCAAGGCTATGCTCTTCACTATGATCAGTACCAAGAAATATATGTG 384
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
DB 385 GACCAAGGCTCGGCTCTGCTCTCTGCACTGGAGGTGGCGGACCAAGTCTGGCTCCAG 444
QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
DB 445 GTGTATGGGAGGAGAGCGTAATGGACTCTATGCTGATGATGATGATGATGATGATGATG 504
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
DB 505 ACAGGCTTCTCTCTACCATGACCAAC 534

RESULT 5
LOCUS AX800354 582 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 14 from Patent WO03055916.
ACCESSION AX800354
VERSION AX800354.1 GI:37653574
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Rasmussen,P.B., Andersen,K.V., Pedersen,A.H., Schambye,H.T.,
AUTHORS Haikier,T. and Bogness,A.
TITLE Adiponectin fragments and conjugates
JOURNAL Patent: WO 03055916-A 14 10-JUL-2003;
Maxygen Aps (DK) ; Maxygen Holdings Ltd. c/o Close Brothers
(Cayman) Limited (KY)
FEATURES
source
Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="apM1(52-244) coding sequence"

ORIGIN
Alignment Scores:
Pred. No.: 2,958-74 Length: 582
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-072-159-11 (1-130) x AX800354 (1-582)

QY 1 PheSerValGlyLeuGluThyValThrIleProAsnMetProIleArgPheThrLys 20
DB 190 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 249
QY 21 IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
DB 250 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGTTAAATTCCTGCAACATT 309
QY 41 ProGlyLeuTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60
DB 310 CTTGGCTGTACTACTTTGGCTACCACTACATCATGATATGAAGGATGTGAAGGTCAGC 369
QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80

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Db      370  CTCTTCAAGAGCAAGGCTATGCTCTTCACTATGATCAGTACCAGGAAAAATAATGTG 429
      |||
QY      81  AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
      |||
Db      430  GACCAGGCTCCGGCTCTGTGCTCTCTGATCTGGAGGTGGGCGACCAAGTCGGCTCCAG 489
      |||
QY      101  ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
      |||
Db      490  GTGTATGGGGAAGGAGCGTAATGACTCTATGCTGATGATGACATGACTCCACCTTC 549
      |||
QY      121  ThrGlyPheLeuLeuTyrHisAspThrAsn 130
      |||
Db      550  ACAGGCTTCTCTCTACCATGACCAAC 579
      |||

RESULT 6
AX752056
LOCUS      735 bp      DNA      linear      PAT 20-JUN-2003
DEFINITION      Sequence 21 from Patent WO0303534.
ACCESSION      AX752056
VERSION      AX752056.1 GI:32134172
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS      Scalia, A., Djalynas, D. and Briggs, K.
TITLE      NGZIPA, NGZIP, PGZIPA, and PGZIPD polynucleotides and polypeptides
JOURNAL
Patent: WO 0303534-A 21 24-APR-2003;
Genset S.A. (FR)
FEATURES
source
1..735
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1..735
/feature="unnamed protein product"
/codon_start=1
/protein_id="CAD99168.1"
/db_xref="GI:32134173"
/translation="MELSGAVLLLLALPGHDQETTTQGPVLLPLPKGACTGMWAGIP
GPHNGAPGDRGDGTPGKEKGDPGLIGPKDIDGETGVPAEGPRGPGIGQRKG
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AYHTIVYMKDKVSLFKKXAMLFTYDQYQENNVDAQSGSVLLHLEVGQWQLQVYGE
GERNGLYADNNDSTFTGFLLYHDN"
ORIGIN
Alignment Scores:
Pred. No.:      3.88e-74      Length:      735
Score:      708.00      Matches:      130
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0

US-10-072-159-11 (1-130) x AX752056 (1-735)
QY      1  PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
      |||
Db      343  TTCAGTGGGATGGAGACTTACCTTACTATCCCAACATGCCATTCGCTTTACCAAG 402
      |||
QY      21  IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
      |||
Db      403  ATCTTCTACCAATACGCAAAACCACTATGATGGTCCACTGTAATTCCACTGCAACATT 462
      |||
QY      41  ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
      |||
Db      463  CCTGGGCTGTACTTCTTGGCTACCAACATCACAGTCTATATGAGGATGTGAAGTCCAG 522
      |||
QY      61  LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
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Db      523  CTCTTCAAGAGCAAGGCTATGCTCTTCACTATGATCAGTACCAGGAAAAATAATGTG 582
      |||
QY      81  AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
      |||
Db      583  GACCAGGCTCCGGCTCTGTGCTCTCTGATCTGGAGGTGGGCGACCAAGTCGGCTCCAG 642
      |||
QY      101  ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
      |||
Db      643  GTGTATGGGGAAGGAGCGTAATGACTCTATGCTGATGATGACATGACTCCACCTTC 702
      |||
QY      121  ThrGlyPheLeuLeuTyrHisAspThrAsn 130
      |||
Db      703  ACAGGCTTCTCTCTACCATGACCAAC 732
      |||

RESULT 7
AX800349
LOCUS      735 bp      DNA      linear      PAT 13-OCT-2003
DEFINITION      Sequence 9 from Patent WO03055916.
ACCESSION      AX800349
VERSION      AX800349.1 GI:37653573
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS      Rasmussen, P.B., Andersen, K.V., Pedersen, A.H., Schambye, H.T.,
Halkier, T. and Bogesnes, A.
TITLE      Adiponectin fragments and conjugates
JOURNAL
Patent: WO 03055916-A 9 10-JUL-2003;
Maxygen Aps (DK); Maxygen Holdings Ltd. c/o Close Brothers
(Cayman) Limited (KY)
FEATURES
source
1..735
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/feature="unnamed protein product"
/codon_start=1
/protein_id="CAD99168.1"
/db_xref="GI:32134173"
/translation="MELSGAVLLLLALPGHDQETTTQGPVLLPLPKGACTGMWAGIP
GPHNGAPGDRGDGTPGKEKGDPGLIGPKDIDGETGVPAEGPRGPGIGQRKG
EPGEGAYVRSASFVGLTYVTIPNPIRFKIFYNQNHGDSGKGFHCNIPGLYF
AYHTIVYMKDKVSLFKKXAMLFTYDQYQENNVDAQSGSVLLHLEVGQWQLQVYGE
GERNGLYADNNDSTFTGFLLYHDN"
ORIGIN
Alignment Scores:
Pred. No.:      3.88e-74      Length:      735
Score:      708.00      Matches:      130
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0

US-10-072-159-11 (1-130) x AX800349 (1-735)
QY      1  PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
      |||
Db      343  TTCAGTGGGATGGAGACTTACCTTACTATCCCAACATGCCATTCGCTTTACCAAG 402
      |||
QY      21  IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
      |||
Db      403  ATCTTCTACCAATACGCAAAACCACTATGATGGTCCACTGTAATTCCACTGCAACATT 462
      |||
QY      41  ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
      |||
Db      463  CCTGGGCTGTACTTCTTGGCTACCAACATCACAGTCTATATGAGGATGTGAAGTCCAG 522
      |||
QY      61  LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
      |||
Db      523  CTCTTCAAGAGCAAGGCTATGCTCTTCACTATGATCAGTACCAGGAAAAATAATGTG 582
      |||
QY      81  AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
      |||
Db      583  GACCAGGCTCCGGCTCTGTGCTCTCTGATCTGGAGGTGGGCGACCAAGTCGGCTCCAG 642
      |||
QY      101  ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
      |||
Db      643  GTGTATGGGGAAGGAGCGTAATGACTCTATGCTGATGATGACATGACTCCACCTTC 702
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QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 703 ACAGGCTTTCTCTACCATGACCAAC 732

RESULT 8
AR034253
LOCUS AR034253 1313 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5869330.
ACCESSION AR034253
VERSION AR034253.1 GI:5949858
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1313)
AUTHORS Scherer,P.E. and Iodish,H.F.
TITLE DNA encoding a novel serum protein produced exclusively in adipocytes
JOURNAL Patent: US 5869330-A 6 09-FEB-1999;
FEATURES Location/Qualifiers
source 1. .1313
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 7.68e-74 Length: 1313
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-072-159-11 (1-130) x AR034253 (1-1313)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 415 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCATTCGCTTTACCAAG 474

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 475 ATCTTCTACATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTACTGCAACATT 534

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 535 CCTGGCTGTACTACTTGGCTACCACTATGATGGCTCCACTGGTAAATTCCTACTGCAACATT 594

QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 595 CTCTTCAGAGGACAGGCTATGCTCTTACCTATGATCAGTACCAAGGAAATTAATGTG 654

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 655 GACCAGGCTCCGGCTCTGTCTCTGCATCTGGAGGTGGCGACCAAGTCTGGCTCCAG 714

QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
Db 715 GTGATGGGAGGAGGACGTAATGGACTCTATGCTGTAATGACATGACTCCACCTTC 774

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 775 ACAGGCTTTCTCTACCATGACCAAC 804

RESULT 9
CQ715267
LOCUS CQ715267 4510 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1201 from Patent WO02068579.
ACCESSION CQ715267
VERSION CQ715267.1 GI:42276124
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humaxons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 1201 06-SEP-2002;

FEATURES PE Corporation (NY) (US)

source 1. .4510

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

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Score: 708.00 Matches: 130

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-072-159-11 (1-130) x CQ715267 (1-4510)

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Db 358 TTCAGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCATTCGCTTTACCAAG 417

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40

Db 418 ATCTTCTACATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTACTGCAACATT 477

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60

Db 478 CCTGGCTGTACTACTTTCCTTACCACATCAGCTATATGAAGGATGTAAGGTACG 537

QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80

Db 538 CTCTTCAGAGGACAGGCTATGCTCTTACCTATGATCAGTACCAAGGAAATTAATGTG 597

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100

Db 598 GACCAGGCTCCGGCTCTGTCTCTGCATCTGGAGGTGGCGACCAAGTCTGGCTCCAG 657

QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120

Db 658 GTGATGGGAGGAGGACGTAATGGACTCTATGCTGTAATGACATGACTCCACCTTC 717

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130

Db 718 ACAGGCTTTCTCTCTTACCATGACCAAC 747

RESULT 10

AR138194

LOCUS AR138194 4517 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 9 from patent US 6197930.

ACCESSION AR138194

VERSION AR138194.1 GI:14479703

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4517)

AUTHORS Sheppard,P.O. and Humes,J.M.

TITLE Adipocyte-specific protein homologs

JOURNAL Patent: US 6197930-A 9 06-MAR-2001;

FEATURES Location/Qualifiers

source 1. .4517

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

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Alignment Scores:
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Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 429 ATCTTCTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTACTGCAACATT 488
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 489 CCTGGGCTGTACTACTTTGGCTACCAATCAGCATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548
QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 549 CTCTTCAAGAGGACAGGCTATGCTCTTACCTATGATCAGTACCAAGAAATAATGTG 608
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
Db 609 GACCAGGCTCCGGCTCTGTGCTCTGTCATCTGGAGGTGGGCGACCAAGCTCTGGCTCCAG 668
QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnSerThrPhe 120
Db 669 GTGTATGGGAGGAGAGCGTAAATGACTCTATGCTGATATGACAAATGACTCCACTTC 728
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 729 ACAGGCTTCTCTCTACCATGACACCAAC 758

RESULT 12
AR337311
LOCUS AR337311 4517 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 5 from patent US 6566332.
ACCESSION AR337311
VERSION AR337311.1 GI:33723295
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4517)
AUTHORS Fruebis, J., Erickson, M.R., Yen, F. and Bihain, B.
TITLE OBG3 globular head and uses thereof for decreasing body mass
JOURNAL Patent: US 6566332-A 5 20-MAY-2003;
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source
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/organism="unknown"
/mol_type="genomic DNA"

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Alignment Scores:
Pred. No.: 3.3e-73 Length: 4517
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-072-159-11 (1-130) x AR337311 (1-4517)

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Db 369 TTCAGTGTGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 428
QY 21 IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 429 ATCTTCTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTACTGCAACATT 488
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 489 CCTGGGCTGTACTACTTTGGCTACCAATCAGCATCACAGTCTATATGAAGGATGTGAAGGTCAGC 548
QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 549 CTCTTCAAGAGGACAGGCTATGCTCTTACCTATGATCAGTACCAAGAAATAATGTG 608
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
Db 609 GACCAGGCTCCGGCTCTGTGCTCTGTCATCTGGAGGTGGGCGACCAAGCTCTGGCTCCAG 668

RESULT 11
AR255755
LOCUS AR255755 4517 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 9 from patent US 6482612.
ACCESSION AR255755
VERSION AR255755.1 GI:27304874
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4517)
AUTHORS Sheppard, P.O. and Humes, J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6482612-A 9 19-NOV-2002;
FEATURES
source
1..4517
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/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.3e-73 Length: 4517
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-072-159-11 (1-130) x AR255755 (1-4517)

QY 1 PheSerValGlyLeuGluThrValThrIleProAsnMetProIleArgPheThrIlys 20
Db 369 TTCAGTGTGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 428

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QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
 Db 669 GTGTATGGGAGGAGCGTAATGGACTATGCTGTAATGACAAATGACTCCACCTTC 728

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 729 ACAGGCTTTCTCTCTACCATGACACCAAC 758

RESULT 13
 LOCUS AR343651 4517 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 5 from patent US 6579852.
 ACCESSION AR343651
 VERSION AR343651.1 GI:33739445
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 4517)
 AUTHORS Fruebis, J., Erickson, M.R., Yen-Potin, F. and Bihain, B.
 TITLE OB93 globular head and uses thereof for decreasing body mass
 JOURNAL Patent: US 6579852-A 5 17-JUN-2003;
 FEATURES
 Location/Qualifiers
 1..4517
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 /mol_type="genomic DNA"
 source

ORIGIN
 Alignment Scores:
 Pred. No.: 3.3e-73 Length: 4517
 Score: 708.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-072-159-11 (1-130) x AR343651 (1-4517)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
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QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCACCTGCAACATT 488

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60
 Db 489 CTGGGCTGTACTCTTGGCTACCATCATGATGGCTCCACTGGTAAATTCACCTGCAACATT 548

QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 549 CTCCTCAAGAGGACAGGCTATGCTTTCACCTATGATGATGAGGATGTAAGTGTG 608

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 609 GACCAGGCTCCGGCTCTGTCTCTGCTCATCTGGAGTGGGGCCACCAAGTCTGGCTCCAG 668

QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
 Db 669 GTGTATGGGAGGAGCGTAATGGACTATGCTGTAATGACAAATGACTCCACCTTC 728

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 729 ACAGGCTTTCTCTCTACCATGACACCAAC 758

RESULT 14
 LOCUS AX195211 4517 bp DNA linear PAT 28-AUG-2001
 DEFINITION Sequence 5 from Patent WO0151645.
 ACCESSION AX195211
 VERSION AX195211.1 GI:15385772

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Bihain, B., Erickson, M.R., Fruebis, J. and Yen-Potin, F.

OB93 globular head and uses thereof for decreasing body mass

AUTHORS

Patent: WO 0151645-A 5 19-JUL-2001;

TITLE

GENSET (FR)

JOURNAL

Location/Qualifiers

FEATURES

1..4517

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 3.3e-73 Length: 4517

Score: 708.00 Matches: 130

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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Db

369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 428

QY

21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40

Db

429 ATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCACCTGCAACATT 488

QY

41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60

Db

489 CTGGGCTGTACTCTTGGCTACCATCATGATGGCTCCACTGGTAAATTCACCTGCAACATT 548

QY

61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80

Db

549 CTCCTCAAGAGGACAGGCTATGCTTTCACCTATGATGATGAGGATGTAAGTGTG 608

QY

81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100

Db

609 GACCAGGCTCCGGCTCTGTCTCTGCTCATCTGGAGTGGGGCCACCAAGTCTGGCTCCAG 668

QY

101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120

Db

669 GTGTATGGGAGGAGCGTAATGGACTATGCTGTAATGACAAATGACTCCACCTTC 728

QY

121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130

Db

729 ACAGGCTTTCTCTCTACCATGACACCAAC 758

RESULT 15

AX335029 4517 bp DNA linear PAT 09-JAN-2002

LOCUS

Sequence 5538 from Patent WO0194629.

DEFINITION

AX335029

ACCESSION

AX335029.1 GI:18125748

VERSION

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

Gene sets

Patent: WO 0194629-A 5538 13-DEC-2001;

Avalon Pharmaceuticals (US)

FEATURES

source Location/Qualifiers
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QY	21	IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle	40
DB	429	ATCTTCTACAATCAGCAAAACCACTAATGATGGTCCACTGGTAAATTCACATGCCAACATT	488
QY	41	ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer	60
DB	489	CCTGGGCTGTACTACTTTCCTACCAACATCACAGTCTATATCAGAGGATGTGAGGTCAGC	548
QY	61	LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal	80
DB	549	CTCTTCAAGAAGGACCAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAATAATGTG	608
QY	81	AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln	100
DB	609	GACCAGGCTCCGGCTCTGTGCTCTTCGATCTGGAGTGGGGGACCAAGTCTGGCTCCAG	668
QY	101	ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe	120
DB	669	GTGTATGGGAGAGGAGCGGTAATGGACTCTATGCTGATAATGACAAATGACTCCACCTTC	728
QY	121	ThrGlyPheLeuLeuTyrHisAspThrAsn	130
DB	729	ACAGGCTTTCTCTCTACCATGACCAAC	758

Search completed: December 3, 2004, 11:40:39
Job time : 2362 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
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Title: US-10-072-159-11

Perfect score: 708

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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4	708	100.0	582	15	US-10-325-717-14 Sequence 14, Appl
5	708	100.0	735	15	US-10-325-717-9 Sequence 9, Appl
6	708	100.0	742	16	US-10-379-747-13 Sequence 13, Appl
7	708	100.0	754	16	US-10-379-747-9 Sequence 9, Appl
8	708	100.0	778	16	US-10-379-747-11 Sequence 11, Appl
9	708	100.0	783	16	US-10-379-747-5 Sequence 5, Appl
10	708	100.0	1550	15	US-10-411-120-19 Sequence 19, Appl
11	708	100.0	4517	9	US-09-776-976-5 Sequence 5, Appl
12	708	100.0	4517	9	US-09-758-055-5 Sequence 5, Appl
13	708	100.0	4517	9	US-09-909-547-5 Sequence 5, Appl
14	708	100.0	4517	9	US-09-964-844A-235 Sequence 235, App
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17	708	100.0	4517	16	US-10-285-833-5 Sequence 5, Appl
18	708	100.0	4545	15	US-10-376-460-5 Sequence 5, Appl
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20	708	100.0	20966	9	US-09-776-976-7 Sequence 7, Appl
21	708	100.0	20966	9	US-09-758-055-7 Sequence 7, Appl
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31	699	98.7	537	15	US-10-325-717-69 Sequence 69, Appl
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38	695	92.5	1276	15	US-10-285-833-3 Sequence 3, Appl
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45	645	91.1	1152	16	US-10-379-747-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-325-717-16
; Sequence 16, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Raemussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bogness, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1 (82-244) coding sequence
US-10-325-717-16

Alignment Scores:
Pred. No.: 1,246-88 Length: 492
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-072-159-11 (1-130) x US-10-325-717-16 (1-492)

Qy 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 100 TTCAAGTGGGATGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 159
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 160 ATCTTCTACATCAGCAAAACCACTATGATGCTCCATGGTAAATTCACCTGCACAACT 219
Qy 41 ProGlyLeuTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 220 CCTGGGCTGTACTTCTGCTACCAATCAGATCTATATGAAGGATGTGAAGGTCCAGC 279
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 280 CTCCTCAAGAGGACAAAGGCTATGCTCTCCTATGATATCAGTACCAAGAAATAATGTG 339
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 340 GACCAGGCTCCGGCTCTGCTCTGATCTGGAGGTGGGACCAAGTCTGGCTCCAG 399
Qy 101 ValTyrGlyGluGlyLysGlnGlnAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
Db 400 GTGTATGGGAGGAGAGCGTAAATGACTCTATGCTGATAATGACAATGACTCCACCTTC 459
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 460 ACAGGCTTCTCTCTACCATGACACCAAC 489

RESULT 2

US-10-325-717-65
; Sequence 65, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct encoding Y111N-apM1 (82-244)
US-10-325-717-65

Alignment Scores:
Pred. No.: 1,416-88 Length: 537
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-072-159-11 (1-130) x US-10-325-717-65 (1-537)

Qy 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 145 TTCAAGTGGGATGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 204
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 205 ATCTTCTACATCAGCAAAACCACTATGATGCTCCATGGTAAATTCACCTGCACAACT 264
Qy 41 ProGlyLeuTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 265 CCTGGGCTGTACTTCTGCTACCAATCAGATCTATATGAAGGATGTGAAGGTCCAGC 324
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 325 CTCCTCAAGAGGACAAAGGCTATGCTCTCCTATGATATCAGTACCAAGAAATAATGTG 384
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 385 GACCAGGCTCCGGCTCTGCTCTGATCTGGAGGTGGGACCAAGTCTGGCTCCAG 444
Qy 101 ValTyrGlyGluGlyLysGlnGlnAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
Db 445 GTGTATGGGAGGAGAGCGTAAATGACTCTATGCTGATAATGACAATGACTCCACCTTC 504
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 505 ACAGGCTTCTCTCTACCATGACACCAAC 534

RESULT 3

US-10-325-717-15
; Sequence 15, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 15
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(58-244) coding sequence
US-10-325-717-15

Alignment Scores:
Pred. No.: 1,52e-88 Length: 564
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-072-159-11 (1-130) x US-10-325-717-15 (1-564)
Qy 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 172 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 231
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 232 ATCTTCTACATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTCACTGCAACATT 291
Qy 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 292 CCTGGCTGTACTACTTGGCTACACATCAGATCTATATGAGGATGTGAAGGTGAGC 351
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 352 CTCTTCAAGAGGACAGGCTATGCTCTTCACTATGATCAGTACAGGAAATATATGTG 411
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 412 GACCAGGCTCCGGCTCTGTCTCTGTCATCTGGAGGTGGCGACCAAGTCTGGCTCCAG 471
Qy 101 ValTyrGlyGluGlyGluAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
Db 472 GTGATGGGAGGAGAGCGTAATGGACTCTATGCTGTATGATGACATGACTCCACCTTC 531
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 532 ACAGGCTTCTCTCTACCATGACACCAAC 561

RESULT 4
US-10-325-717-14
; Sequence 14, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: apM1(52-244) coding sequence
US-10-325-717-14

Alignment Scores:
Pred. No.: 1,59e-88 Length: 582
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-072-159-11 (1-130) x US-10-325-717-14 (1-582)
Qy 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 190 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG 249
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 250 ATCTTCTACATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTCACTGCAACATT 309
Qy 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 310 CCTGGCTGTACTACTTGGCTACACATCAGATCTATATGAGGATGTGAAGGTGAGC 369
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 370 CTCTTCAAGAGGACAGGCTATGCTCTTCACTATGATCAGTACAGGAAATATATGTG 429
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 430 GACCAGGCTCCGGCTCTGTCTCTGTCATCTGGAGGTGGCGACCAAGTCTGGCTCCAG 489
Qy 101 ValTyrGlyGluGlyGluAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
Db 490 GTGATGGGAGGAGAGCGTAATGGACTCTATGCTGTATGATGACATGACTCCACCTTC 549
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 550 ACAGGCTTCTCTCTACCATGACACCAAC 579

RESULT 5
US-10-325-717-9
; Sequence 9, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/412,169
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Homo sapiens
```

FEATURE:
OTHER INFORMATION: apM1 (1-244) coding sequence
US-10-325-717-9

Alignment Scores:
Pred. No.: 2,26e-88 Length: 735
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-072-159-11 (1-130) x US-10-325-717-9 (1-735)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 343 TTCAGTGTGGGATGGAGACTTACGTTACTATCCCAACATGCCCAATCGCTTTACCAAG 402
QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 403 ATCTTCTACATCAGCAAAACCACTATGATGCTCCACTGGTAAATTCCTGCAACATT 462
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 463 CTGGGCTGTACTACTTTCCTCCACCATCAGCTATATGAGGATGTGAAGGTCCAGC 522
QY 61 LeuPheLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 523 CTCCTCAAGAGACAGGCTATGCTTCTACCTATGATCAGTACCAAGAAATTAATGTG 582
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 583 GACCAGGCTCCGGCTCTGCTCTCGCATCTGGAGTGGGGACCAAGTCTGGCTCCAG 642
QY 101 ValTyrGlyGluGlyGluArgGlnGlyLeuTyrAlaAspAsnAspAsnSerThrPhe 120
Db 643 GTGTATGGGAGAGAGAGGCTAATGGACTCTATGCTGATGATAATGACATGACTCCACCTTC 702
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 703 ACAGGCTTCTTCTCTTACCATGACACCAAC 732

RESULT 6

US-10-379-747-13
Sequence 13, Application US/10379747
Publication No. US20040023874A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.;
APPLICANT: Chant, John S.;
APPLICANT: Chaudhuri, Amitabha ;
APPLICANT: Edinger, Shlomit R.;
APPLICANT: Gangolli, Esha A.;
APPLICANT: Malyankar, Uriel M.;
APPLICANT: Miller, Charles E.;
APPLICANT: Ooi, Chean Eng.;
APPLICANT: Ort, Tatiana A.;
APPLICANT: Patturajan, Meera ;
APPLICANT: Rastelli, Luca ;
APPLICANT: Rieger, Daniel K.;
APPLICANT: Shinkets, Richard A.;
APPLICANT: Zerkhusen, Bryan D.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-568B
CURRENT APPLICATION NUMBER: US/10/379,747
PRIOR FILING DATE: 2003-03-05
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/365,034
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/365,477
PRIOR FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Curasequid version 0.1

SEQ ID NO 13
LENGTH: 742
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (11)..(709)
US-10-379-747-13
Alignment Scores:
Pred. No.: 2,29e-88 Length: 742
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-072-159-11 (1-130) x US-10-379-747-13 (1-742)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
Db 320 TTCAGTGTGGGATGGAGACTTACGTTACTATCCCAACATGCCCAATCGCTTTACCAAG 379
QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 380 ATCTTCTACATCAGCAAAACCACTATGATGCTCCACTGGTAAATTCCTGCAACATT 439
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
Db 440 CTGGGCTGTACTACTTTCCTCCACCATCAGCTATATGAGGATGTGAAGGTCCAGC 499
QY 61 LeuPheLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 500 CTCCTCAAGAGACAGGCTATGCTTCTACCTATGATCAGTACCAAGAAATTAATGTG 559
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 560 GACCAGGCTCCGGCTCTGCTCTCGCATCTGGAGTGGGGACCAAGTCTGGCTCCAG 619
QY 101 ValTyrGlyGluGlyGluArgGlnGlyLeuTyrAlaAspAsnAspAsnSerThrPhe 120
Db 620 GTGTATGGGAGAGAGAGGCTAATGGACTCTATGCTGATGATAATGACATGACTCCACCTTC 679
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 680 ACAGGCTTCTTCTCTTACCATGACACCAAC 709

RESULT 7

US-10-379-747-9
Sequence 9, Application US/10379747
Publication No. US20040023874A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.;
APPLICANT: Chant, John S.;
APPLICANT: Chaudhuri, Amitabha ;
APPLICANT: Edinger, Shlomit R.;
APPLICANT: Gangolli, Esha A.;
APPLICANT: Malyankar, Uriel M.;
APPLICANT: Miller, Charles E.;
APPLICANT: Ooi, Chean Eng.;
APPLICANT: Ort, Tatiana A.;
APPLICANT: Patturajan, Meera ;
APPLICANT: Rastelli, Luca ;
APPLICANT: Rieger, Daniel K.;
APPLICANT: Shinkets, Richard A.;
APPLICANT: Zerkhusen, Bryan D.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-568B
CURRENT APPLICATION NUMBER: US/10/379,747
PRIOR FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: 60/365,034
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/366,420

```

; CURRENT APPLICATION NUMBER: US/10/379,747
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/365,034
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/366,420
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/365,477
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 11
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(766)
US-10-379-747-11

Alignment Scores:
Pred. No.: 2,46e-88 Length: 778
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-072-159-11 (1-130) x US-10-379-747-11 (1-778)
Qy 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrIys 20
Db 377 TTTCAGTGGGAGATTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTTACCAAG 436
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 437 ATCTTCTCAATATCAGAAAACCACTATGATGGCTCCACTGGTNAATTCACCTGCACATT 496
Qy 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValIysValSer 60
Db 497 CQTGGGCTGTACTACTTTGGCTACCAATCACAGTCATATATGAAGGATGTGAAGGTGACG 556
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
Db 557 CTCCTTCAAGAGGACAAAGGCTATGCTCTTCCACTATGATCAGTACGAGGAAATATATGG 616
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 617 GACCAAGGCTCCGGCTCTGTCTCTGCACTCGAGGTGGGACCAAGCTGGCTCCAG 676
Qy 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
Db 677 GTGTATGGGAGGAGAGCGTAATGGACTCTATGCTGATAATGACAATGACTCCACCTTC 736
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db 737 ACAGGCTTCTTCTTACCATGACCAAC 766

RESULT 9
US-10-379-747-5
; Sequence 5, Application US/10379747
; Publication No. US20040023874A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.;
; APPLICANT: Chant, John S.;
; APPLICANT: Chaudhuri, Amitabha ;
; APPLICANT: Edinger, Shlomit R.;
; APPLICANT: Gangolli, Esha A.;
; APPLICANT: Malvankar, Uriel M.;
; APPLICANT: Miller, Charles E.;
; APPLICANT: Ooi, Chean Eng;
; APPLICANT: Ort, Tatiana A.;
; APPLICANT: Patturajan, Meera ;
; APPLICANT: Rastelli, Luca ;

```

; APPLICANT: Rieger, Daniel K.;
; APPLICANT: Shimkets, Richard A.;
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCES: 21402-568B
; CURRENT APPLICATION NUMBER: US/10/379,747
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/365,034
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/366,420
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/365,477
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 5
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(743)
US-10-379-747-5

Alignment Scores:

Pred. No.:	2,49e-88	Length:	783
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-10-072-159-11 (1-130) x US-10-379-747-5 (1-783)

Qy	1	PheserValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys	20
Db	354	TTCAAGTGTGGATTTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG	413
Qy	21	IlePheTyrAsnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle	40
Db	414	ATCTTCAATCAGCAAAACCACTATGATGCTCCATCGTAAATTCACATGCAACATT	473
Qy	41	ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer	60
Db	474	CCTGGGCTGTACTTCTTCCCTACCACATCAGCTCTATATGAAGGATGTGAAGTCCAG	533
Qy	61	LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal	80
Db	534	CTCTTCAAGAGGACAAAGCTATGCTTTCACCTATGATCAGTACCAAGAAATATATGTG	593
Qy	81	AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln	100
Db	594	GACCAAGGCTCCGGCTCTGTCTCTGCTATCGGAGTGGGCGACCAAGTCTGGCTCCAG	653
Qy	101	ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe	120
Db	654	GTGTATGGGGAAGGAGGAGGTAATGGACTCTATGCTGTAATGACATGACTCCACCTTC	713
Qy	121	ThrGlyPheLeuLeuTyrHisAspThrAsn	130
Db	714	ACAGGCTTTCTTCTTACCATGACACCAAC	743

RESULT 10

US-10-411-120-19
; Sequence 19, Application US/10411120
; Publication No. US20030224425A1
; GENERAL INFORMATION:
; APPLICANT: Blondel et al.
; TITLE OF INVENTION: ACRP-30-like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: FT316P1
; CURRENT APPLICATION NUMBER: US/10/411,120
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/328,419

; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US02/32432
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 19
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1547)..(1547)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-411-120-19

Alignment Scores:

Pred. No.:	6.96e-88	Length:	1550
Score:	708.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-10-072-159-11 (1-130) x US-10-411-120-19 (1-1550)

Qy	1	PheserValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys	20
Db	384	TTCAAGTGTGGATTTGGAGACTTACGTTACTATCCCAACATGCCCATTCGCTTTACCAAG	443
Qy	21	IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle	40
Db	444	ATCTTCAATCAGCAAAACCACTATGATGCTCCATCGTAAATTCACATGCAACATT	503
Qy	41	ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer	60
Db	504	CCTGGGCTGTACTTCTTCCCTACCACATCAGCTCTATATGAAGGATGTGAAGTCCAG	563
Qy	61	LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal	80
Db	564	CTCTTCAAGAGGACAAAGCTATGCTTTCACCTATGATCAGTACCAAGAAATATATGTG	623
Qy	81	AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln	100
Db	624	GACCAAGGCTCCGGCTCTGTCTCTGCTATCGGAGTGGGCGACCAAGTCTGGCTCCAG	683
Qy	101	ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe	120
Db	684	GTGTATGGGGAAGGAGGAGGTAATGGACTCTATGCTGTAATGACATGACTCCACCTTC	743
Qy	121	ThrGlyPheLeuLeuTyrHisAspThrAsn	130
Db	744	ACAGGCTTTCTTCTTACCATGACACCAAC	773

RESULT 11

US-09-776-976-5
; Sequence 5, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: CBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US4.REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881

;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: Patent.pm
;; SEQ ID NO 5
;; LENGTH: 4517
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-776-976-5

Alignment Scores:
Pred. No.: 3,49e-87 Length: 4517
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-072-159-11 (1-130) x US-09-776-976-5 (1-4517)

Qy 1 PheSerValGlyLeuGluThrTyrValThrLeuProAsnMetProIleArgPheThrLys 20
|||
Db 369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCAATTCGCTTTACCAAG 428
|||
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
|||
Db 429 ATCTTCTACATCAGCAAAACACATGATGCTCCCTGCTGTAATTCCTGCTGCAACATT 489
|||
Qy 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
|||
Db 489 CTGGGCTGTACTTTCCTTGCCTACCATCAGCTATATGAAGGATGTGAAGGTCCAGC 548
|||
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnLysAsnVal 80
|||
Db 549 CTCITTCAGAGGAGGACGAGCTATGCTCTTCCCTATGATGATGATGATGATGATGATG 609
|||
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
|||
Db 609 GACCAGGCTCCGGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
|||
Qy 101 ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
|||
Db 669 GTGTATGGGAGGAGGAGCGTAAATGGACTCTATGCTGTAATGTAATGTAATGTAATGTA 728
|||
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
|||
Db 729 ACAGGCTTCTCTCTACCATGACCAAC 758
|||

RESULT 12

US-09-758-055-5
; Sequence 5, Application US/09758055
; Patent No. US20020058617A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76 US 4 REG
; CURRENT APPLICATION NUMBER: US 09/758,055
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 4517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-758-055-5

Alignment Scores:

Pred. No.: 3,49e-87 Length: 4517
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-072-159-11 (1-130) x US-09-758-055-5 (1-4517)

Qy 1 PheSerValGlyLeuGluThrTyrValThrLeuProAsnMetProIleArgPheThrLys 20
|||
Db 369 TTCAGTGTGGGATTGGAGACTTACGTTACTATCCCAACATGCCCAATTCGCTTTACCAAG 428
|||
Qy 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
|||
Db 429 ATCTTCTACATCAGCAAAACACATGATGCTCCCTGCTGTAATTCCTGCTGCAACATT 488
|||
Qy 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
|||
Db 489 CTGGGCTGTACTTTCCTTGCCTACCATCAGCTATATGAAGGATGTGAAGGTCCAGC 548
|||
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnLysAsnVal 80
|||
Db 549 CTCITTCAGAGGAGGACGAGCTATGCTCTTCCCTATGATGATGATGATGATGATGATG 608
|||
Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
|||
Db 609 GACCAGGCTCCGGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
|||
Qy 101 ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspAspSerThrPhe 120
|||
Db 669 GTGTATGGGAGGAGGAGCGTAAATGGACTCTATGCTGTAATGTAATGTAATGTAATGTA 728
|||
Qy 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
|||
Db 729 ACAGGCTTCTCTCTACCATGACCAAC 758
|||

RESULT 13

US-09-909-547-5
; Sequence 5, Application US/09909547
; Patent No. US20020091080A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76 US 6 CIP
; CURRENT APPLICATION NUMBER: US 09/909,547
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 4517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-547-5

Alignment Scores:

Pred. No.: 3,49e-87 Length: 4517
Score: 708.00 Matches: 130

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-072-159-11 (1-130) x US-09-909-547-5 (1-4517)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
DB 369 TTCAGTGTGGATTGGAGACTTACGTACTATCCCAACATGCCATTGCGTTTACCAAG 428
QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
DB 429 ATCTTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTGCAACATT 488
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60
DB 489 CTTGGGCTGTACTCTTTCCTACCAATCAGTCTATATGAGGATGTGAGGTCCAGC 548
QY 61 LeuPheLysAspLysAlaMetLeupheThrTyrAspGlnTyrGlnGluAsnVal 80
DB 549 CTCTTCAAGAAGACAGAGGTATGCTCTTCACTATGATCAGTACCAAGAAATTAATGTG 608
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
DB 609 GACCAGGCTCCGGCTCTGTCTCTCGCATCTGGAGGTGGCGGACCAAGTCTGGCTCCAG 668
QY 101 ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
DB 669 GTGTATGGGAGGAGGAGGTATGCTCTTCACTATGATCAGTACCAAGTCTGGCTCCAG 728
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
DB 729 ACAGGCTTTCTCTTCTACCATGACACCAAC 758

RESULT 14

US-09-964-824A-235
; Sequence 235, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 4517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-235

Alignment Scores:
Pred. No.: 3,49e-87 Length: 4517
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-072-159-11 (1-130) x US-09-964-824A-235 (1-4517)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
DB 369 TTCAGTGTGGATTGGAGACTTACGTACTATCCCAACATGCCATTGCGTTTACCAAG 428

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
DB 429 ATCTTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTGCAACATT 488
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60
DB 489 CTTGGGCTGTACTCTTTCCTACCAATCAGTCTATATGAGGATGTGAGGTCCAGC 548
QY 61 LeuPheLysAspLysAlaMetLeupheThrTyrAspGlnTyrGlnGluAsnVal 80
DB 549 CTCTTCAAGAAGACAGAGGTATGCTCTTCACTATGATCAGTACCAAGAAATTAATGTG 608
QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
DB 609 GACCAGGCTCCGGCTCTGTCTCTCGCATCTGGAGGTGGCGGACCAAGTCTGGCTCCAG 668
QY 101 ValTyrGlyGluGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
DB 669 GTGTATGGGAGGAGGAGGTATGCTCTTCACTATGATCAGTACCAAGTCTGGCTCCAG 728
QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
DB 729 ACAGGCTTTCTCTTCTACCATGACACCAAC 758

RESULT 15

US-10-231-814-5
; Sequence 5, Application US/10231814
; Publication No. US20030100500A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76,US4,REG
; CURRENT APPLICATION NUMBER: US/10/231,814
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 4517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-231-814-5

Alignment Scores:
Pred. No.: 3,49e-87 Length: 4517
Score: 708.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-10-072-159-11 (1-130) x US-10-231-814-5 (1-4517)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
DB 369 TTCAGTGTGGATTGGAGACTTACGTACTATCCCAACATGCCATTGCGTTTACCAAG 428
QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
DB 429 ATCTTACAAATCAGCAAAACCACTATGATGGCTCCACTGGTAAATTCCTGCAACATT 488
QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValSer 60

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Db      |||||CTGGGCTGTACTACTTTGGCTTACCACATCACAGTCTATATGAAGGATGTGAAGTCAAGC 548
QY      |||||LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnAsnVal 80
Db      |||||549 CTCCTCAGAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAAAAATAATGTG 608
QY      |||||81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTriLeuGln 100
Db      |||||609 GACCAGGCTCCGGCTCTGTGCTCTCGATCTGGAGGTGGGGGACCAAGTCTGGCTCCAG 668
QY      |||||101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
Db      |||||669 GTGTATGGGGAAGGAGAGCGTAATGGACTCTATGCTGATGATAATGACATGACTCCACCTTC 728
QY      |||||121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
Db      |||||729 ACAGGCTTCTTCTCTACCATGACACCAAC 758
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Job time : 401 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2004, 09:59:48 ; Search time 2971 Seconds
(without alignments)
1594.468 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGLTYTIPNPIRFTK.....YADNNDSTFTGFLLYHDTN 130

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=EST -QFMT=fastap -SURFLX=p2n.rst -MINWATCH=0.1 -LOOPCF=0 -LOPEXT=0
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-DALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
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2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	661	93.4	610	2	AW915595 EST346899
4	661	93.4	857	7	CO389083 AGENCOURT
5	655	92.5	523	5	BX519230 BX519230
6	655	92.5	523	2	BE625509 uul19e06.Y
7	655	92.5	566	1	AA028544 mi18b08.r
8	655	92.5	921	3	AK003138 Mus muscu
9	655	92.5	1158	3	AK041214 Mus muscu

C	10	652	92.1	605	4	BM384395
	11	647	91.4	545	1	AI158610
	12	638	90.1	1465	3	BC078720
	13	637	90.0	543	1	AI105446
C	14	636	89.8	577	5	BQ189822
	15	634	89.5	811	1	AA763396
C	16	634	89.5	905	1	AI747241
	17	609	86.0	921	1	AA673154
	18	604	85.3	508	1	AA493090
	19	582	82.2	885	1	AI323115
	20	574	81.1	856	5	BQ876848
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	22	568	80.2	830	7	CF843149
	23	558	78.8	468	2	AW988554
	24	558	78.8	634	7	CO384703
C	25	556	78.5	600	1	AA960123
	26	555	78.4	694	2	BE225356
	27	551	77.8	786	7	CO400150
	28	549	77.5	438	1	AA061943
C	29	548	77.4	486	2	BE626169
C	30	544.5	76.9	585	1	AI323469
	31	537	75.8	468	2	AW911832
	32	537	75.8	470	2	AW986727
	33	537	75.8	519	2	BE478076
	34	533	75.3	707	4	BG872725
C	35	510	72.0	433	1	AI407605
	36	501	70.8	758	6	CF345349
	37	501	70.8	787	6	CF345350
	38	496	70.1	445	1	AI171410
	39	492	69.5	867	7	CF376220
	40	490	69.2	406	4	BG090627
	41	475.5	67.2	766	7	CO387981
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ALIGNMENTS

RESULT 1

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LOCUS

DEFINITION

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BC054496

BC054496

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Db      1828  CCTGGCTGTACTACTTTGGCTACCACATCACAGCTATATGAAGGTGTGAAGTCAGC 1769
Qy      61  LeuPheLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
1768  CTCCTTCAAGAGGACAGAGCTATGCTCTTCCATCATGATCAGTACCAGGAAATATATGTG 1709
Qy      81  AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
1708  GACCAAGGCTCCGGCTCTGTGCTCTCTGATCTGGAGTGGCGACCAAGCTGCTGCTCCAG 1649
Qy      101  ValTyrGlyGluGlyGluAlaAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
1648  GTGTATGGGAGAGAGAGCGTAATGGACTATGCTGATATGATGACATGACTCCACCTTC 1589
Qy      121  ThrGlyPheLeuLeuTyrHisAspThrAsn 130
1588  ACAGGCTTCTCTCTACCATGACACCAAC 1559

RESULT 3
LOCUS   AW915595
DEFINITION EST346899 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
RGIC17 5' end, mRNA sequence.
ACCESSION AW915595
VERSION   AW915595.1 GI:8081296
KEYWORDS EST.
SOURCE   Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 610)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1999)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@igrr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.

FEATURES
source
1..610
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RGIC17"
/dev_stages="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"

ORIGIN
Alignment Scores:
Pred. No.: 1.59e-74 Length: 610
Score: 661.00 Matches: 120
Percent Similarity: 96.9% Conservative: 6
Best Local Similarity: 92.31% Mismatches: 4
Query Match: 93.36% Indels: 0
DB: 2 Gaps: 0

US-10-072-159-11 (1-130) x AW915595 (1-610)
Qy      1  PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrIys 20
Db      58  TTCAGGTAGGCTGGAGCCCGCTCACTGTCCTCCATGTTCCTCCATCGTTTACTAAG 117
Qy      21  IlePheTyrAsnGlnGluAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40

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Db      118  ATCTTCTACACCAACAGCAATCATATGACGCGACAGCTGGCAATTCCTCACTGCACATT 177
Qy      41  ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
178  CCGGGCTCTTACTACTTTTCTACCACATCAGCGGTGTACATGAAGGATGTGAAGTGAGC 237
Qy      61  LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
238  CTCTTCAAGAGGACAGGCGGTCTCTTCCATCTGACACCATGATCAGGAAAAATATGTG 297
Qy      81  AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100
298  GACCAAGGCTCTGCTCCATGCTCTCCATCTGGAGTGGGAGACCAAGTCTGGCTCCAA 357
Qy      101  ValTyrGlyGluGlyGluAlaAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
358  GTGTATGGGAGGAGGACCAACATGACTCTATGACAGATATGTCATGACTCTACATT 417
Qy      121  ThrGlyPheLeuLeuTyrHisAspThrAsn 130
418  ACAGGCTTCTCTCTACCATGATACCAAC 447

RESULT 4
LOCUS   CO389083
DEFINITION IMAGE:7304566 5', mRNA sequence.
ACCESSION CO389083
VERSION   CO389083.1 GI:49496674
KEYWORDS EST.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 857)
AUTHORS NIH-MGC http://mgi.nhl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabps@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (LILNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LILNL at:
http://image.lilnl.gov
Plate: LILNL15341 row: f column: 20
High quality sequence stop: 644.
FEATURES
source
1..857
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7304566"
/tissue_type="Ovary - Brown Norway Line 3 Age 8 weeks.
Tissues were snap-frozen and transferred in -70c. RNase
free the entire procedure."
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_253"
/note="Organ: ovary; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from female animals at 8 wk
old. Tissues were snap-frozen and kept at -80C for two
days before RNA extraction and purification (TRI-reagent
method). cDNA was primed using oligo-dT primer:
5'-PGACTAGTCTAGATCGGCGGCCCTT-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.2kb
resulted in an average insert size of 1.5 kb. This primary

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library is normalized (non-normalized primary library is NIH_MGC_252) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 2,45e-74 Length: 857
 Score: 661.00 Matches: 120
 Percent Similarity: 96.92% Conservative: 6
 Best Local Similarity: 92.31% Mismatches: 4
 Query Match: 93.36% Indels: 0
 DB: 7 Gaps: 0

US-10-072-159-11 (1-130) x C0389083 (1-857)

Qy 1 PheSerValGlyLeuGluThrTyrrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 69 TTCAGGCTAGGGCTGGAGACCCGCGTCACTGCCCAATGTTCCCATTCGCTTACTAAG 128
 Qy 21 IlePheTyrrAsnGlnGlnAsnHisTyrrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 129 ATCTTCTACAAACCAAGAAATCATATGACGGCAGCACTGGCAAAATTCACATGCAACATT 188
 Qy 41 ProGlyLeuTyrrPheAlaTyrrHisIleThrValTyrrMetLysAspValLysValSer 60
 Db 189 CCGGGGCTCTACTACTTCTTCTTACCACATCAGCGGTGTACATGAAGATGTGAAGTGAGC 248
 Qy 61 LeuPheLysAspLysAlaMetLeuPheThrTyrrAspGlnTyrrGlnGluAsnVal 80
 Db 249 CTCCTCAAGAGGACCAAGCCGCTCTCTTCCCTACGACCATATCAGAAATAAATGTG 308
 Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 309 GACCAAGCTCTGGCTCCATGCTCTCCATCTGGAGTGGGAGACCAAGTCTGGCTCCA 368
 Qy 101 ValTyrrGlyGluGlyGluArgAsnGlyLeuTyrrAlaAspAsnAspAsnAspSerThrPhe 120
 Db 369 GTGTATGGGAGGAGGACCAACATGACATCTATGACAGATAATGTCAATGACTCTACATT 428
 Qy 121 ThrGlyPheLeuLeuTyrrHisAspThrAsn 130
 Db 429 ACAGGCTTCTTCTTCTTACCATGATACCAAC 458

RESULT 5
 BX519230 523 bp mRNA linear EST 27-JUN-2003
 LOCUS BX519230 Soares mammary gland NMLMG Mus musculus cDNA clone
 DEFINITION IMAGE:3372418 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
 complement-related protein Acrp30 (MOUSE);, mRNA sequence.

ACCESSION BX519230.1 GI:32300580
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 523)
 Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
 and Korn, B.
 Mouse Unigeneset - R2PD2
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE998D213139.
 RZPDLiB; I.M.A.G.E. cDNA Clone Collection;
 Mouse Unigeneset - R2PD2 (RZPDLiB No.981)
 http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 T7, Primer sequence: TAATACGACTCACTATAGGG.

FEATURES

source

1..523

/organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE998D213139 ; IMAGE:1247588"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /clone_lib="Soares mammary gland NMLMG"
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from mammary
 gland tissue from a lactating female, and was then primed
 with a Not I - cligo(dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified pT73 vector. Library is normalized. Library
 was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 7.75e-74 Length: 523
 Score: 655.00 Matches: 119
 Percent Similarity: 96.92% Conservative: 7
 Best Local Similarity: 91.54% Mismatches: 4
 Query Match: 92.51% Indels: 0
 DB: 5 Gaps: 0

US-10-072-159-11 (1-130) x BX519230 (1-523)

Qy 1 PheSerValGlyLeuGluThrTyrrValThrIleProAsnMetProIleArgPheThrLys 20
 Db 88 TTCAGTGTGGGCTGGAGACCCGCGTCACTGTCCCAATGTCCCAATTCGCTTACTAAG 147
 Qy 21 IlePheTyrrAsnGlnGlnAsnHisTyrrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 148 ATCTTCTACAAACCAAGAAATCATATGACGGCAGCACTGGCAAAATTCACATGCAACATT 207
 Qy 41 ProGlyLeuTyrrPheAlaTyrrHisIleThrValTyrrMetLysAspValLysValSer 60
 Db 208 CCGGGGCTCTACTACTTCTTACCACATCAGCGGTGTACATGAAGATGTGAAGTGAGC 267
 Qy 61 LeuPheLysAspLysAlaMetLeuPheThrTyrrAspGlnTyrrGlnGluAsnVal 80
 Db 268 CTCTTCAGAGAGGACCAAGCCGCTTCTTCCCTACGACCATATCAGGAAAGATGTG 327
 Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 328 GACCAAGCTCTGGCTCTGTGCTCTCCATCTGGAGTGGGAGACCAAGTCTGGCTCCA 387
 Qy 101 ValTyrrGlyGluGlyGluArgAsnGlyLeuTyrrAlaAspAsnAspAspSerThrPhe 120
 Db 388 GTGTATGGGATGGGACCAACATGACATCTATGACAGATAACGTCAACGACTCTACATT 447
 Qy 121 ThrGlyPheLeuLeuTyrrHisAspThrAsn 130
 Db 448 ACTGGCTTCTTCTTCTTACCATGATACCAAC 477

RESULT 6

LOCUS

DEFINITION

BX625509 552 bp mRNA linear EST 24-AUG-2000
 uui9806.y1 Soares mammary gland NMLMG Mus musculus cDNA clone
 IMAGE:3372418 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
 complement-related protein Acrp30 (MOUSE);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 552)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1082022
 Seq primer: -40RP from Gibco
 High quality sequence stop: 486.
 Location/Qualifiers
 1..552
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:3372418"
 /sex="female (lactating)"
 /tissue_type="mammary gland"
 /lab_host="DH10B"
 /clone_lib="Soares mammary gland NMLMG"
 /note="Vector: pTV3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from mammary
 gland tissue from a lactating female, and was then primed
 with a Not I - oligo(dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified pTV73 vector. Library is normalized. Library
 was constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 8,296-74 Length: 552
 Score: 655.00 Matches: 119
 Percent Similarity: 96.92% Conservative: 7
 Best Local Similarity: 91.54% Mismatches: 4
 Query Match: 92.51% Indels: 0
 DB: 2 Gaps: 0

US-10-072-159-11 (1-130) x BE262509 (1-552)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 DB 97 TTCAGTGTGGGCTGAGACCGCGTCACTGTCCCAATGACCAATTCGCTTACTAAG 156
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 157 ATCTTCTACACCAACAGAAATCATATATGACGGCAGCACTGGCAAGTTCCTACTGCAACATT 216
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 DB 217 CCGGACTCTACTCTCTCTTCCACATCATCGGTGTACATGAAAGATGTGAAGTGAGC 276
 QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 DB 277 CTCTTCAAGAGGACACAGCGCGTCTCTTCCCTACGACCACTATCAGAAAGATGTG 336
 QY 81 AspGlnAlaSerGlySerValLeuLeuHisIleGluValGlyAspGlnValTyrLeuGln 100
 DB 337 GACCAAGGCTCTGGCTCTGTCTCTCCATCTGGAGGTGGAGACCAAGTCTGCTCCAG 396
 QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspAsnAspSerThrPhe 120
 DB 397 GTGTATGGGATGGGACCAACATGATCTATGACAGATACGTCACGACTCTACATT 456
 QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 DB 457 ACTGGCTTCTCTCTACCATGATACCAAC 486

RESULT 7

AA028544

LOCUS

DEFINITION

AA028544 566 bp mRNA linear EST 11-SEP-1996
 m18008.r1 Soares mouse p3NNF19.5 Mus musculus cDNA clone
 IMAGE:463863 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
 complement-related protein Acrp30 (MOUSE);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 8,566-74 Length: 566
 Score: 655.00 Matches: 119
 Percent Similarity: 96.92% Conservative: 7
 Best Local Similarity: 91.54% Mismatches: 4
 Query Match: 92.51% Indels: 0
 DB: 1 Gaps: 0

US-10-072-159-11 (1-130) x AA028544 (1-566)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 DB 28 TTCAGTGTGGGCTGAGACCGCGTCACTGTCCCAATGACCAATTCGCTTACTAAG 87
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 88 ATCTTCTACACCAACAGAAATCATATATGACGGCAGCACTGGCAAGTTCCTACTGCAACATT 147
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60

ORIGIN

Alignment Scores:

Pred. No.: 8,566-74 Length: 566
 Score: 655.00 Matches: 119
 Percent Similarity: 96.92% Conservative: 7
 Best Local Similarity: 91.54% Mismatches: 4
 Query Match: 92.51% Indels: 0
 DB: 1 Gaps: 0

US-10-072-159-11 (1-130) x AA028544 (1-566)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 DB 28 TTCAGTGTGGGCTGAGACCGCGTCACTGTCCCAATGACCAATTCGCTTACTAAG 87
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 88 ATCTTCTACACCAACAGAAATCATATATGACGGCAGCACTGGCAAGTTCCTACTGCAACATT 147
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60

ORIGIN

Alignment Scores:

Pred. No.: 8,566-74 Length: 566
 Score: 655.00 Matches: 119
 Percent Similarity: 96.92% Conservative: 7
 Best Local Similarity: 91.54% Mismatches: 4
 Query Match: 92.51% Indels: 0
 DB: 1 Gaps: 0

US-10-072-159-11 (1-130) x AA028544 (1-566)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20
 DB 28 TTCAGTGTGGGCTGAGACCGCGTCACTGTCCCAATGACCAATTCGCTTACTAAG 87
 QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 DB 88 ATCTTCTACACCAACAGAAATCATATATGACGGCAGCACTGGCAAGTTCCTACTGCAACATT 147
 QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60

RESULT 7

AA028544

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
 Db 444 ATCTTCTACAAACAGAGATCATTTATGACGCGACACTGGCAAGTCTCTACGCACTT 503

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60
 Db 504 CCGGGACTCTACTCTCTCTTACCAACATCACGGTGTACATGAAGATGTGAAGGTGAGC 563

QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80
 Db 564 CTCTTCAAGAAGACAGACGCGTCTCTCTTCACTACGACCATGATCAGGAAAGATGTG 623

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
 Db 624 GACGAGCTCTGCTGCTCTCTCTCCATCTGCGAGGTGGAGACCAAGCTCGGTCCAG 683

QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120
 Db 684 GTGTATGGGATGGGACCAATGCACTCTATGAGATACGTCACGCACTCTACATTT 743

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130
 Db 744 ACTGGCTTTCTCTCTTACCATGATACCAAC 773

RESULT 9
 AK041214
 LOCUS DEFINITION
 Mus musculus adult male aorta and vein cDNA, RIKEN full-length
 enriched library, clone:A53009P11 product:adipocyte complement
 related protein of 30 kDa, full insert sequence.

ACCESSION
 VERSION AK041214.1 GI:26334296
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed capillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE
 4 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 695-690 (2001)

REFERENCE
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation

JOURNAL
 REFERENCE
 AUTHORS

of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1158)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanegaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saibto, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.

TITLE
 JOURNAL

Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0845, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.

FEATURES

source

1. 1158
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM,DB:A53009P11"
 /db_xref="taxon,10090"
 /cdate="A53009P11"
 /sex="male"
 /tissue_type="aorta and vein"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
 65. 7808
 /codon_start=1
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 /db_xref="GI:26334297"
 /translation="MLLLQALLPLLLPSHAEDDVTTTELAPALVPPPKGTGAGWMA
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 RKGEGLAAVYVRSAFSGVLETRVTVPVIRPTKIFINQNHGDSGTGKFCYNIPGL
 YFSEYHETVMKDVKVSFLKDKKAVLFYDYQEKVNDQASGVLLHLEVGDOVLQV
 YGDDHNGLYADVNDSTFTGFLYHDTN"

CDS

/note="unnamed protein product; adipocyte complement
 related protein of 30 kDa (MGD|MG1:106675, GI|NM_009605,
 evidence: BLASTN, 99%, match=744)
 putative"

ORIGIN

Alignment Scores:
 Pred. No.: 2,128-73 Length: 1158
 Score: 655.00 Matches: 119
 Percent Similarity: 96.92% Conservative: 7
 Best Local Similarity: 91.54% Mismatches: 4
 Query Match: 92.51% Indels: 0
 DB: 3 Gaps: 0

US-10-072-159-11 (1-130) x AK041214 (1-1158)

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20

Db 416 TTCAGTGTGGGCTGGAGACCCGCGTCACTGTGCCAATGTACCATTCGCTTACTAAG 475

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40

Db 247 GACGAGGCTCTGGCTCTGCTCTCCATCTGGAGGTGGAGACCAAGTCTGGCTCCAG 306

QY 101 ValTyrGlyGluGlyGluArgenGlyLeuTyrAlaAspAsnAspSerThrPhe 120

Db 307 GTGTATGGGATGGGACCAACATGACTCTATGCAGATAACGTCAACGACTCTACATT 366

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130

Db 367 ACTGGCTTCTCTACCATGATACCAAC 396

RESULT 12

BC078720 1465 bp mRNA linear HTC 03-AUG-2004

LOCUS Rattus norvegicus cDNA clone IMAGE:7109244, containing frame-shift errors.

DEFINITION BC078720

ACCESSION BC078720.1 GI:50927299

VERSION BC078720.1

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 1465)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, F.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.B., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 1465)

AUTHORS Director MGC Project.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Howard Jacobs

CNA Library Preparation: Express Genomics

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 181 Row: 1 Column: 7

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21426808

This clone has the following problem: frame shifted.

Location/Qualifiers

source

1. 1465

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="IMAGE:7109244"

/tissue_type="Kidney, rat (Brown Norway)"

/clone_lib="NIH_MGC_235"

/lab_host="DH10B"

/note="Vector: pExpress1"

ORIGIN

Alignment Scores: Length: 1465

Pred. No.: 638.00 Matches: 120

Score: 96.92% Conservative: 6

Percent Similarity: 92.31% Mismatches: 4

Best Local Similarity: 90.11% Indels: 1

Query Match: 3 Gaps: 0

DB: 3

US-10-072-159-11 (1-130) x BC078720 (1-1465).

QY 1 PheSerValGlyLeuGluThrTyrValThrIleProAsnMetProIleArgPheThrLys 20

Db 383 TTCAGCGTAGGCGTGGAGACCGCGTCACTGTCCCAATGTCCCATTCGCTTTACTAAG 442

QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40

Db 443 ATCTTCACCAACCAAGATCATTTATGCGGAGCACTGGCAATTCCTGCTGCACATT 502

QY 41 ProGlyLeuTyrTyrPheAlaTyrHisIleThrValTyrMetLysAspValLysValSer 60

Db 503 CCGGGGCTTCTACTTCTTCTCCACCATCACCGTGTACATGAAGGATGTGAAAGTGAGC 562

QY 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnVal 80

Db 563 CTCTTCAAGAGGAGGCGGCTCTCTTCCCTACCATCATCAGGATATCAGGAAAAA-AATGTG 621

QY 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGln 100

Db 622 GACAGGCTTCTGCTCTCATCTCTTCACTGGAGTGGAGACCAAGTCTGGCTCCAA 681

QY 101 ValTyrGlyGluGlyGluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPhe 120

Db 682 GTGTATGGGAGGAGGACCAACATGAGTCTATGCAGATAATGTCATGACTCTACATT 741

QY 121 ThrGlyPheLeuLeuTyrHisAspThrAsn 130

Db 742 ACAGGCTTCTTCTCTACCATGATACCAAC 771

RESULT 13

LOCUS A1105446/c

DEFINITION EST214735 Normalized rat kidney, Bonto Soares Rattus sp. cDNA clone R18K49 3' end, mRNA sequence.

ACCESSION A1105446

VERSION A1105446.1 GI:3709525

KEYWORDS EST.

SOURCE Rattus sp.

ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 543)

AUTHORS Lee, N.H., Glodex, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R., and Adams, M.D.

TITLE Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat Gene Index

JOURNAL Unpublished (1998)

COMMENT Other ESTs: TC52707

Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

BEST AVAILABLE COPY

Fax: (301)-838-0208
Email: mhlee@igr.org
Seq primer: M13-21

FEATURES

source

Location/Qualifiers
1..543
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2030555"
/db_xref="taxon:10118"
/clone="RK18K49"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: Kidney; Vector: pT73Pac; Site_1: EcoRI;
Site_2: NotI"

ORIGIN

Alignment Scores:
Pred. No.: 1,69e-71 Length: 543
Score: 637.00 Matches: 115
Percent Similarity: 96.80% Conservative: 6
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 89.97% Indels: 0
DB: 1 Gaps: 0

US-10-072-159-11 (1-130) x A1105446 (1-543)

QY 6 GluThrTyrValThrIleProAsnMetProIleArgPheThrLysIlePheTyrAsnGln 25
DB 529 GAGACCCGGCTCAGTGTCCCAATGTTCCCATTCGCTTACTAGACTTCTTACAACCA 470
QY 26 GlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIleProGlyLeuTyrTyr 45
DB 469 CAGATCATTATGACGGCAGCACTGGCAATTCCTGCACTGCACATTCGGGGCTCTACTAC 410
QY 46 PheAlaTyrHisIleThrValTyrMetLysAspValLysValSerLeuPheLysLysAsp 65
DB 409 TTTTCTTACCACATCACGCTGTACATGAAGATGTGAAAGTGAGGCTCTTCAAGAGGAC 350
QY 66 LysAlaMetLeuPheThrTyrAspGlnTyrGlnGluAsnValAspGlnAlaSerGly 85
DB 349 AAGCGCGTCTCTTCCCTACACAGATCAGGAAAAATGTGGACCGGCTCTGTGC 290
QY 86 SerValLeuLeuHisLeuGluValGlyAspGlnValTyrLeuGlnValTyrGlyGluGly 105
DB 289 TCCATGCTCTCCATCTGAGGTGGAGACCAAGTCTGGCTCCAAGTGTATGGGAGGG 230
QY 106 GluArgAsnGlyLeuTyrAlaAspAsnAspSerThrPheThrGlyPheLeuLeu 125
DB 229 GACACAAAGGACTATGACAGATAATGTCAATGACTCTACATTACAGGCTTCTTCTC 170
QY 126 TyrHisAspThrAsn 130
DB 169 TACCATGATACCAAC 155

RESULT 14
BQ189822/c
LOCUS
DEFINITION
BQ189822 linear EST 30-APR-2002
UI-R-CN1-cjn-e-02-0-UI-s3 UI-R-CN1 Rattus norvegicus cDNA clone
UI-R-CN1-cjn-e-02-0-UI 3', mRNA sequence.
BQ189822.1 GI:20365373
VERSION
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 577)
REFERENCE
AUTHORS
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
9704477
PUBMED
8889548

Contact: Soares, MS
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brown adipose library cDNA Library Preparation: M.B. Soares Lab Clone Distribution: clones will be available through Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1..577
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CN1-cjn-e-02-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CN1"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not-I; Site_2: Eco RI; The UI-R-CN1
library is a subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat penis, normalized rat
bladder, normalized rat cervix, normalized rat brown
adipose, normalized rat fundus, and normalized rat
salivary gland. It was constructed according to the
procedures described by Bonaldo, Lennon & Soares (Genome
Research 6: 791-806, 1996). For construction of
the CN1 library, plasmid DNA from the pool of normalized
libraries was electroporated into competent bacteria for
the production of single-stranded circular DNA. This was
then used as a tracer in a subtractive hybridization with
a driver (PCR amplified inserts from a plasmid DNA template
preparation) comprising: a) a pool of about 34,000 clones
from the Rat Unigene Set corresponding to plates R-5-AA-NN
excluding plates R-5-MM and MN. This pool represented 40%
of the final driver population. b) a pool of about 29,000
clones from subtracted libraries CA0 and CA1 corresponding
to plates R-CA0-AW through R-CA0-AXS, R-CA0-AZX through
R-CA0-BAZ, R-CA0-BPE through R-CA0-BHY, R-CA0-BJS,
R-CA0-BKE, R-CA0-BKG-M, R-CA0-BKT-K, R-CA0-BKP through
R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
R-CA0-BOU, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through
R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR,
R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF,
R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through
R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and
R-CA1-BLE. The resulting pool represented 24% of the
final driver population. c) a pool of about 15,000 clones
from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s
and normalized libraries CS0, CT0, CU0, CW0, and CX0
corresponding to plates R-CT0s-CAX, R-CU0s-CBP through
R-CT0s-CAM through R-CT0s-CBD through R-CW0s-CCB, R-
CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN
through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through
R-CS0-BTV, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP,
R-CT0-BVN, R-CU0-BUQ through R-CU0-BVL, R-CW0-BVY through
R-CW0-BWP, R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through
R-CX0-BXW. The resulting pool represented 5% of the final
driver population. d) a pool of about 5,000 clones (1,000
from non-normalized eye library CV0 and 4,000 from
normalized eye library CV1) corresponding to plates
R-CV0-BRH through R-CV0-BRR, R-CV1-BRS through R-CV1-BSC,

FEATURES

source

R-CV1-BSE through R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool represented about 5% of the final driver population. e) A pool of about 10,000 clones from subtracted library BS2, BV0 and BVOP (7-9.5 kb cDNA library fraction from rat whole embryo), and BX0 (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to plates R-BS2-BDE through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BVOP-AOI through R-BVOP-AOX, and R-BX0-AQY through R-BX0-ASH. The resulting pool represented 5% of the final driver population. f) A pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including C10, C20, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DD0-BYQ through R-DD0-CBA, R-DD0-BZR through R-DD0-CAA, R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population. g) A pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKW through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) A pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-09-0-UI, bkw-b-11-0-UI, bkw-b-10-0-UI, bkw-d-01-0-UI, bkw-d-06-0-UI, bkw-g-08-0-UI, bkw-h-12-0-UI, bky-a-05-0-UI, bkg-a-06-0-UI, bkg-a-11-0-UI, bkg-c-06-0-UI, bkg-c-09-0-UI, bkg-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI, bla-h-12-0-UI, bla-i-02-0-UI, bla-i-11-0-UI, bla-e-95-0-UI, bla-l-08-0-UI, bla-f-02-0-UI, bla-g-04-0-UI, bla-r-05-0-UI, bla-f-02-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkg-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.

TAG TISSUE=brown adipose
TAG LIB=UI-R-CN1
TAG_SEQ=TTGTC"

ORIGIN

Alignment Scores:
Pred. No.: 2,45e-71 Length: 577
Score: 636.00 Matches: 116
Percent Similarity: 94.62% Conservatives: 7
Best Local Similarity: 89.23% Mismatches: 7
Query Match: 89.83% Indels: 0
DB: 5 Gaps: 0

US-10-072-159-11 (1-130) x BQ189822 (1-577)

Qy 1 PheSerValGlyLeuGluThrTyrrValThrIleProAsnMetProIleArgPheThrLys 20
Db 570 TTACGCTAGGCTGGAGACCCGGTCACGTGCCCAATGTTCCCATTCGTTACTACG 511
Qy 21 IlePheTyrrAsnGlnAsnHisTyrrAspGlySerThrGlyLysPheHisCysAsnIle 40
Db 510 ATCTTCAAGACCAACAGATCATTTATGACGGGACGACTGGCAATTCACATGCAACATT 451
Qy 41 ProGlyLeuTyrrTyrrPheAlaTyrrHisIleThrValTyrrMetLysAspValLysValSer 60
Db 450 CCGGGGCTCTAATCTTTTCTTACCACATCATCCGCTGACATGAGATGTGAAGTGACG 391
Qy 61 LeuPheLysLysAspLysAlaMetLeuPheThrTyrrAspGlnTyrrGlnGluAsnVal 80
Db 390 CTCTTCAAGAGGACCAAGCCGCTCTCTTCCACCTAGCACCAGTATCAGGAAAAAATGTG 331

Qy 81 AspGlnAlaSerGlySerValLeuLeuHisLeuGluValGlyAspGlnValTrpLeuGln 100
Db 330 GACCAGGCTCTGCTGCTCCATCTCTCCATCTCTGAGGTGGAGACCAAGTCTGGCTCCAA 271
Qy 101 ValTyrrGlyGluGlyGluArgAsnGlyLeuTyrrAlaAspAsnAspAsnAspSerThrPhe 120
Db 270 GTGTATGGGAGAGGAGGACCAATGACCTATGCGAGATATGTCATGACTCTACATTT 211
Qy 121 ThrGlyPheLeuLeuTyrrHisAspThrAsn 130
Db 210 ACAGGCTCTCTCTCTACCATGATACCAAC 181

RESULT 15

AA763396

LOCUS

DEFINITION

AA763396

ACCESION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA763396 811 bp mRNA linear EST 27-JAN-1998
vW53g11.r1 Soares mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1247588 5' similar to gb:U37222 Mus musculus 30kDa adipocyte
complement-related protein Acrp30 (MOUSE);, mRNA sequence.

AA763396 GI:2813143
AA763396.1
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 811)
Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LInL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:661276

Putative full length read
vector to vector length is 849
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 470.
Location/Qualifiers
1..811
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1247588"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland_NMLMG"
/notes="vector: p77T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p77T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES

source

location

qualifiers

1..811

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1247588"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/clone_lib="Soares mammary_gland_NMLMG"

/notes="vector: p77T3D-Pac (Pharmacia) with a modified
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High quality sequence stop: 470.

Location/Qualifiers

1..811

/organism="Mus musculus"

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/db_xref="taxon:10090"

/clone="IMAGE:1247588"

/sex="female (lactating)"

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ORIGIN

Alignment Scores:
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Score: 634.00 Matches: 119
Percent Similarity: 96.32% Conservatives: 7
Best Local Similarity: 91.54% Mismatches: 4
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DB: 1 Gaps: 0

US-10-072-159-11 (1-130) x AA763396 (1-811)

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Db 57 TTCAGTGTGGGGTGGAGCCG- GTCACATGTTCCCAATGTACCCATCGCTTACTAAG 115
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QY 21 IlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheHisCysAsnIle 40
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Db 176 CCGGACTCTTACTACTTCTCTTACCACATCACCGTGTACATGAAGATGTGAAGGTGAGC 235
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